

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: May 10, 2003, 23:15:14 ; Search time 238 Seconds

(Without alignments)
67.994 Million cell updates/sec

Title: US-09-905-657-2

Perfect score: 2848

Sequence: 1 MGRSNEODLSTELVNRGIE.....KKPTRRNPWDICINRYPVL 550

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2845	99.9	550	4 US-08-868-373-8	Sequence 8, Appli
2	1569	55.1	516	4 US-08-868-373-14	Sequence 14, Appl
3	1493	52.4	537	4 US-08-868-373-10	Sequence 10, Appl
4	1446.5	50.8	500	4 US-08-868-373-12	Sequence 12, Appl
5	1445	50.7	497	4 US-08-868-373-2	Sequence 4, Appli
6	1438	50.5	520	4 US-08-868-373-2	Sequence 4, Appli
7	1194	41.9	493	4 US-08-868-373-2	Sequence 2, Appli
8	1186	41.6	506	3 US-08-868-988-2	Sequence 2, Appli
9	1186	41.6	506	4 US-08-868-373-6	Sequence 6, Appli
10	1170.5	41.1	504	4 US-08-868-988-4	Sequence 4, Appli
11	334	11.7	127	3 US-08-362-633-4	Sequence 4, Appli
12	334	11.7	127	4 US-08-362-633-4	Sequence 5, Appli
13	169.5	6.0	349	4 US-08-994-035C-5	Sequence 5, Appli
14	169.5	6.0	349	4 US-08-994-035C-5	Sequence 5, Appli
15	166.5	5.8	349	4 US-08-994-035C-5	Sequence 5, Appli
16	166.5	5.8	349	4 US-08-994-035C-5	Sequence 5, Appli
17	151.5	5.3	333	4 PCT-US96-10986-12	Sequence 12, Appl
18	148.5	5.2	83	4 US-08-145-828A-2	Sequence 3946, Ap
19	125.5	4.4	394	4 US-08-252-816A-1	Sequence 2, Appli
20	113	4.0	1094	2 US-08-680-326-40	Sequence 1, Appli
21	102	3.6	420	4 US-09-213-053-4	Sequence 40, Appl
22	102	3.6	1394	4 US-09-213-053-2	Sequence 4, Appli
23	97.5	3.4	324	1 US-08-746-797-2	Sequence 2, Appli
24	97.5	3.4	324	1 US-08-927-387-2	Sequence 2, Appli
25	97.5	3.4	324	1 US-08-918-058-2	Sequence 2, Appli
26	96.5	3.4	307	4 US-09-134-001C-5144	Sequence 5144, Ap
27	96	3.4	903	2 US-08-209-521-24	Sequence 24, Appl

28	96	3.4	903	4 US-08-961-810-134	Sequence 134, App
29	96	3.4	903	4 US-08-352-902D-134	Sequence 134, App
30	95.5	3.4	682	1 US-07-998-003A-107	Sequence 107, App
31	95.5	3.4	682	1 US-08-453-274B-107	Sequence 107, App
32	95.5	3.4	682	1 US-08-453-695A-107	Sequence 107, App
33	95.5	3.4	682	1 US-08-268-161A-107	Sequence 107, App
34	95.5	3.4	682	2 US-08-453-702A-107	Sequence 107, App
35	95.5	3.4	682	4 US-09-099-639-107	Sequence 107, App
36	95.5	3.4	682	5 PCT-US93-12588-107	Sequence 107, App
37	95.5	3.4	682	5 PCT-US95-08071-107	Sequence 107, App
38	95.5	3.4	836	1 US-07-998-003A-105	Sequence 105, App
39	95.5	3.4	836	1 US-08-453-274B-105	Sequence 105, App
40	95.5	3.4	836	1 US-08-453-695A-105	Sequence 105, App
41	95.5	3.4	836	1 US-08-268-161A-105	Sequence 105, App
42	95.5	3.4	836	2 US-08-453-702A-105	Sequence 105, App
43	95.5	3.4	836	5 US-09-099-639-105	Sequence 105, App
44	95.5	3.4	836	5 PCT-US93-12588-105	Sequence 105, App
45	95.5	3.4	836	5 PCT-US95-08071-105	Sequence 105, App

ALIGNMENTS

RESULT 1					
US-08-868-373-8					
Sequence 8, Application US/08868373					
Patent No. 6307128					
GENERAL INFORMATION:					
APPLICANT: JAWORSKI, Jan G.					
APPLICANT: Post-Beitlenmiller, Martha A.					
TITLE OF INVENTION: FATTY ACID ELONGASIS					
FILE REFERENCE: 07148/064001					
CURRENT APPLICATION NUMBER: US/08/868.373					
CURRENT FILING DATE: 1997-06-03					
NUMBER OF SEQ ID NOS: 22					
SOFTWARE: FASTSEQ for Windows Version 3.0					
SEQ ID NO 8					
LENGTH: 550					
TYPE: PRT					
ORGANISM: Arabidopsis thaliana					
US-08-868-373-8					
Query Match					
Best Local Similarity 99.9% Score 2845; DB 4; Length 550;					
Matches 549; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MGRSNEODLSTELVNRGIEPSGPNAGSPTESVRRRLPDFLOSINKYVLAGHYLIN	60	Sequence 134, App	
DB	1	MGRSNEODLSTELVNRGIEPSGPNAGSPTESVRRRLPDFLOSINKYVLAGHYLIN	60	Sequence 107, App	
QY	61	HAVYATPVLVLFVSAEVSLSREIWKIMDYDLATVIGFVFLTACYEFSRPRS	120	Sequence 107, App	
DB	61	HAVYATPVLVLFVSAEVSLSREIWKIMDYDLATVIGFVFLTACYEFSRPRS	120	Sequence 107, App	
QY	121	VYLIDFACVKSDEKVKKEEFLARKSGKDEETLGFKKILQASGIDETVPRIS	180	Sequence 107, App	
DB	121	VYLIDFACVKSDEKVKKEEFLARKSGKDEETLGFKKILQASGIDETVPRIS	180	Sequence 107, App	
QY	181	SEENITTKKEGEEASTYIFGALDELFEKTRVKKPDVGVLYVNCISIFNPTSLAMVINH	240	Sequence 107, App	
DB	181	SEENITTKKEGEEASTYIFGALDELFEKTRVKKPDVGVLYVNCISIFNPTSLAMVINH	240	Sequence 107, App	
QY	241	YKMRGNIISYNGMGCSAGIADLADMLQSNNSAVVSTVMGVNMTVSGDKSMV	300	Sequence 107, App	
DB	241	YKMRGNIISYNGMGCSAGIADLADMLQSNNSAVVSTVMGVNMTVSGDKSMV	300	Sequence 107, App	
QY	301	IPNCFRMGCSAVMISNRPRFRAKRYLEHVFHKAADRSFVSVOEEDGEGFKGLK	360	Sequence 105, App	
DB	301	IPNCFRMGCSAVMISNRPRFRAKRYLEHVFHKAADRSFVSVOEEDGEGFKGLK	360	Sequence 105, App	
QY	361	ISRDLMEVGEALKTNTITLGLVLPFSEQLFRFPAKSTSTTSTSTATA	420	Sequence 105, App	
DB	361	ISRDLMEVGEALKTNTITLGLVLPFSEQLFRFPAKSTSTTSTSTATA	420	Sequence 105, App	

Db 361. ISRDLMFVGEALTKNTITLGLPLVPSEQLLEFPAALVYRRTSPAKTSTTSTSTATA 420
Qy 421. KTGKSSSSDLSPYIPDYKLAPEHFCFHAASVYLEELOKNLGSEENNEASRMTLHR 480
Db 421. KTGKSSSSDLSPYIPDYKLAPEHFCFHAASVYLEELOKNLGSEENNEASRMTLHR 480
Qy 481. FGNWSSGIVYELAYMAKESVRRGDRVWQJAFSGFKCSVYKAKRYKPKPRNPVW 540
Db 481. FGNWSSGIVYELAYMAKESVRRGDRVWQJAFSGFKCSVYKAKRYKPKPRNPVW 540
Qy 541. DCINRYPVPL 550
Db 541. DCINRYPVPL 550

RESULT 2

US-08-868-373-14
; Sequence 14, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868,373
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-868-373-14

Query Match 55.1%; Score 1569; DB 4; Length 516;
Best Local Similarity 56.5%; Pred. No. 3.3e-155;
Matches 300; Conservative 82; Mismatches 117; Indels 32; Gaps 5;

Qy 23. GPNAGSPFVSRYRRRLPDLQSVNLKYGKGYHLYLNHAYVLATIPVLVFSAEVSL 82
Db 13. GGGGDSVGVQIRQTRMLPDLQSVNLKYGKGYHLYLNHAYVLATIPVLVFSAEVSL 71
Qy 83. SREIWKRLM---DYDLATVIGFGVFLVTAQVYFMSRPRSVYLIDFCYRPSDEHKATK 139
Db 72. NPDDL-KQLWHLQYLVNLSIICSAIIVFGITVYVTRPRVYLVDFSCYLPDLKAPY 130
Qy 140. EEFELARKSGKDEDETLGFKRILLOASGIDETVYVPRSSISENITMKEGREASTVI 199
Db 131. ARFMSHRLTGDFDSDSLFQKILERSGLGEDTYVPEAMHYVPRISMAAREBAEQVM 190
Qy 200. FGALDELFEKTRVYKGVYVNCSTFNPPLSLAMVINHYKRGNTLSYNLGMCOSA 259
Db 191. FGALDINFPANTVYKPDIGILVNCSTFNPPLSLAMVINHYKRGNTLSYNLGMCOSA 250
Qy 260. GIIAIDLARDMLQSNPVSVAVVSTEMVGYNMVYVSDSKSVIIPCFRMCSSAVMLSNRR 319
Db 251. GVIAYLADLAKMLLVHRTYAVVSTENITQWYFNGKSMILPCLERVGSAAVLISNKS 310
Qy 320. RDRHAKYRLHEHYVTHKAADRSFRSVYOEDQGFGLKISIDLMVEGVALKTNTIT 379
Db 311. RDRRSRYRLVHYVTHRGADKAFRCVYOEDQGTGTVSLSDMLAIGELTKNTIT 370
Qy 380. LGLPLVPSEQLLEFPAALVYRRTSPAKTSTTSTSTATAKNGIKSSSSDLSPYIPD 439
Db 371. LGLPLVPISQILFEMTVL-----VKKLNGVYKPYIPD 404
Qy 440. YKLAPEHFCFHAASVYLEELOKNLGSEENNEASRMTLHREGNTSSGIVYELAYWEAK 499
Db 405. FKLAFEHFCIHAGRAVIDELEKNLQSPVHYEASRMTLHREGNTSSGIVYELAYWEAK 464
Qy 500. ESVYRGDRVWQJAFSGFKCSVYKAKRYKPKPRNPVWDCINRYVPL 550
Db 500. ESVYRGDRVWQJAFSGFKCSVYKAKRYKPKPRNPVWDCINRYVPL 550

Db 465. GRMRGNRVWQJAFSGFKCSAIVEALRVY-KPSNNSPWEDCIDKYPVPL 514

RESULT 3

US-08-868-373-10
; Sequence 10, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868,373
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-868-373-10

Query Match 52.4%; Score 1493; DB 4; Length 537;
Best Local Similarity 52.6%; Pred. No. 3.1e-147;
Matches 287; Conservative 103; Mismatches 116; Indels 40; Gaps 9;

Qy 12. TELVNRGIEPSPGNAGSPFVSRYV---RRRLPDLQSVNLKYGKGYHLYLNHAYVLAT 67
Db 23. SEAMEANRP--VNGGS--VQIRTEENERRKLPNFIQSVNMKMYKGYHLYLHFKCL 78
Qy 68. IPLVLYFSAEYGSLSREIWKRLM---DYDLATVIGFGVFLVTAQVYFMSRPRSVYL 124
Db 79. VPLVLYFSAEYGSLSREIWKRLM---DYDLATVIGFGVFLVTAQVYFMSRPRSVYL 136
Qy 125. DEACKYRPSDEHKATKEEFELARKSGKDEDETLGFKRILLOASGIDETVYVPRSSISEN 184
Db 137. DYCSTLPESLQVYKQKFMDSKLEDEPNESLEFQKILERSGLGEDTYVPEAMHYVPRIS 196
Qy 165. ITTMEGDEASTVIYFGALDELFEKTRVYKGVYVNCSTFNPPLSLAMVINHYKMR 244
Db 197. RPTMAAREEEOVMFGLDKLFENTKINPRDIGLVVNCSTFNPPLSLAMVINHYKMR 256
Qy 245. GIIISYNLGMCOSAGIIAIDLARDMLQSNPVSVAVVSTEMVGYNMVYVSDSKSVIIPNC 304
Db 257. GNVKSFNLGMCOSAGVSIIDLAKDMLVHRTYAVVSTENITQWYFNGKSMILPCLERV 316
Qy 305. FFRMGCSAVMLSNRRDPFRHAKYRLHEHYVTHKAADRSFRSVYOEDQGFGLKISID 364
Db 317. LFRVGSAILLSNKGDRRSKRYLVHRTYHKAADRSFRSVYOEDQGTGTVSLSDMLAIG 376
Qy 365. LMEVGEALKTNTITLGLPLVPSEQLLEFPAALVYRRTSPAKTSTTSTSTATAKNG 424
Db 377. LMAIAGALKANITTYLPLVLPISQILFEMTVLTK----- 412
Qy 425. IKSSSDLSKPYIPDYKLAPEHFCFHAASVYLEELOKNLGSEENNEASRMTLHREGNT 484
Db 413. KLFNSKL-KPYIPDYKLAPEHFCIHAGRAVIDELEKNLQSPVHYEASRMTLHREGNT 470
Qy 485. SSSGIVYELAYWEAKESVRRGDRVWQJAFSGFKCSVYKAKRYKPKPRNPVWDCIN 544
Db 471. SSSSIVYELAYWEAKGKMKRGVWQJAFSGFKCSAVVAVLNNV-KPSVSSPWEHCID 529
Qy 545. RYVPL 550
Db 530. RYVPL 535

RESULT 4

US-08-868-373-12
; Sequence 12, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:

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us-09-905-657-2.raii

Page 3

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: APPLICANT: Jaworski, Jan G.
: APPLICANT: Post-Beltemmiller, Marcha A.
: APPLICANT: Todd, James
: TITLE OF INVENTION: FATTY ACID ELONGASES
: FILE REFERENCE: 07148/064001
: CURRENT APPLICATION NUMBER: US/08/868,373
: CURRENT FILING DATE: 1997-06-03
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 12
: LENGTH: 500
: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
US-08-868-373-12

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Query Match	50.8%;	Score 1446.5;	DB 4;	Length 500;
Best Local Similarity	53.3%;	Pred. No. 2e-142;		
Matches 281; Conservative	94;	Mismatches 111;	Indels 41;	Gaps 9;

[illegible][illegible]

QY	323	RHXYBLEHIVYTHKADDDRSFVYQDEBDCQKGLKISNDLMEVGEALKNITTLGP	3623
DB	294	WRAKIKLSHVRKIRGADDSFYCYVYQDEDEGHVGNLSLDMAIENGKAKATITIGP	3533
QY	383	LVLPFEOLLFPALL--RRTFSPAKSTYTTTSFSTSAFTANGIKSSSDLSKRYIPDYK	4411
DB	354	LVLPASOLLFLVTSLIKRINPK-----WKRYIDDFK	3666

[illegible]

RESULT 5
 US-09-058-947A-4
 Sequence 4, Application US/09058947A
 Patent No. 6274790
 GENERAL INFORMATION:
 APPLICANT: Kunst et al.
 TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
 TITLE OF INVENTION: Involved In Very Long Chain Fatty Acid Synthesis
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:

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ZIP: 97204-2988
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Word97 & ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,947A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/043,831
FILING DATE: April 14, 1997
ATTORNEY/AGENT INFORMATION:
NAME: David J. Earp, Ph.D.
REGISTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 5493-50032/DJE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
? ?
US-09-058-947A-4

Query Match 50.7% Score 1445; DB 4; Length 497;
Best Local Similarity 53.9%; Pred. No. 2.9e-142;
Matches 278; Conservative 93; Mismatches 107; Indels 38; Gaps 8;

Query Match	50.7%;	Score 1445;	DB 4;	Length 497;
Best Local Similarity	53.9%;	Pred. NO. 2.9e-142;		
Matches 278;	Conservative 93;	Mismatches 107;	Indels 38;	Gaps 8;

[illegible][illegible][illegible][illegible]

RESULT 6
US-08-868-373-2
; Sequence 2, Application US/08868373
Patent No. 6307128

```

; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868,373
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-868-373-2

```

```

Query Match
Best Local Similarity 50.5%; Score 1438; DB 4; Length 520;
Matches 285; Conservative 96; Mismatches 123; Indels 50; Gaps 10;

```

```

QY 6 EDDLSTELVNGIEPSGNSGPFVSVRRLDPLFOSVNLKYKLGHYHLINHA-- 63
DB 2 DBERITAEKAFR-----DSSSAVIRIRRLDPLTSVKLYKGLHNSCNTTLL 52
QY 64 -YLATIP---VLVLFSAEVSLSREIIM-KKIMDYDIAVIG--FFGVFLTACVPM 115
DB 53 FFLILPLPLGVLTQLTGTFDFTFS--ELMSQAVQLODRTATLTCLVLSFVLT--LYVA 108
QY 116 SPPRSVYILDFACYPSPDEHKYTKKEFEELAKSKSPDEETLGFKRILQASIGDETV 175
DB 109 NNSKPEVYLVDFSCYKPEDEKRIKISVDSFLMTEENGSEFTDDYVQFOORISNRAIGDETV 168
QY 176 PRSISSENIITMKEGREASVIFGALDELFEKTRVVKDVGVLVYVNCSTNPPTSLSA 235
DB 169 PRGITSTPKLMSARAEAEVAFMGALDSFEKTKIGKPAEGLIIVNCSLEPNPTSLSA 228
QY 236 MVINHYKRNKGNLISYNLGMCAGIITADLADMLQSNPNSTAYAVVSTENYVMMYYS 295
DB 229 MIVNHYKRNKREDIKSYNLGMCAGIITADLADMLQSNPNSTAYAVVSTENYVMMYYS 288
QY 296 DKSMTYPCFRMGCSAVMLSNRRDPFRHAKYRLHIVTRHKAADRSFRSYQDEDEG 355
DB 289 DRSMCLNCIIFRMGAAILLSNRQDRKSKSYLVNVRTHGSDOKNVCYQKEDERG 348
QY 356 FKGLKISDLMEVGEALKTNTTIGPLVLPSEQLLFFPALLRKTFSPAKTSTTTSFS 415
DB 349 TIGVSLAEMLSVAGDAKLTNTTIGPLVLPSEQLLFFPALLRKTFSPAKTSTTTSFS 393
QY 416 TSAFAKTNGIKSSSDLSKPYIPDYKLAFEHCFHAKSKVVLLEIQLKMLGSEENMEAS 475
DB 394 -----KMEKTK-----VKPYIPDCKLAFEHCFHAGRAVLDEYQKMLDKDMMEPSR 442
QY 476 MTLHRFGTSSGTYELAYWEAKESVARGRWQVQIAFGSFKCNSVYKAKRYK-RPT 534
DB 443 MTLHRFGTSSGTYELAYWEAKESVARGRWQVQIAFGSFKCNSVYKAKRYK-RPT 502
QY 535 RNNPWCINRYPV 548
DB 503 TGNMAGSIDQPV 516

```

```

RESULT 7
US-08-868-373-4
; Sequence 4, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868,373
; CURRENT FILING DATE: 1997-06-03

```

```

; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-868-373-4

```

```

Query Match
Best Local Similarity 41.9%; Score 1194; DB 4; Length 493;
Matches 235; Conservative 97; Mismatches 141; Indels 40; Gaps 8;

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```

QY 48 LKVKIGHYILNHAVYLAFTIPVLVLSAEVGSLSREIIMKLMYD---DLATVIGFPG 104
DB 5 MKKVKIFFEYVLAHREKLCFLPLMAV-I-AVEASRLSTQDL-QNFVLYLQNNHTSLMFPL 62
QY 105 VFVLTCVYEMSPRSVYILDFACYPSPDEHKYTKKEFEELAKSKSPDEET---LG 158
DB 63 YIALGSTLYLMTKPKVYLVDFSCYLPSPHLASTQRIHQHVLVNEAGAMQESDYLM 122
QY 159 FKRILQASIGDETVPRSSISENITMKEGREASVIFGALDELFEKTRVVKDVG 218
DB 123 FCKILERSGLQGETVYVPEGLQTLPLQNLAVSRIETEEVILGAVDNLFRTNGISPDIG 182
QY 219 VLVYVNCSTNPPTSLSAMVINHYKRNKGNLISYNLGMCAGIITADLADMLQSNPN 278
DB 183 ILVYVNCSTNPPTSLSISYVNFKRLDNIKISYNLGMCAGIITADLADMLQSNPN 242
QY 279 AVVSTENYVMMYYSKPYIPDYKLAFEHCFHAKSKVVLLEIQLKMLGSEENMEAS 338
DB 243 ALVSTENTQVLMQNNKSMVYVNCSTNPPTSLSAMVINHYKRNKGNLISYNLGMCAGI 302
QY 339 ADRESFRSYQDEDEGFKGLKISDLMEVGEALKTNTTIGPLVLPSEQLLFFPAL 398
DB 303 ADRESFRSYQDEDEGFKGLKISDLMEVGEALKTNTTIGPLVLPSEQLLFFPAL 362
QY 399 RPTF-SPAKTSTTTSFSATAKTNGIKSSSDLSKPYIPDYKLAFEHCFHAKSKVYL 457
DB 363 KKKFLNPKL-----KHVYIPDCKLAFEHCFHAGRAVL 395
QY 458 EELQKMLGSEENMEASRMTLHRFGTSSGTYELAYWEAKESVARGRWQVQIAFGSGF 517
DB 396 DMEKRNHLITPLDVASRMTLHRFGTSSGTYELAYWEAKESVARGRWQVQIAFGSGF 455
QY 518 KNSVYKAKRYK-RPT 550
DB 456 KNSVYKAKRYK-RPT 487

```

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RESULT 8
US-08-868-998-2
; Sequence 2, Application US/08888998
; Patent No. 6124524
; GENERAL INFORMATION:
; APPLICANT: JAMES, Douglas W.
; APPLICANT: LIM, Eda
; APPLICANT: KELLER, Janis
; APPLICANT: DOONER, Hugo K.
; TITLE OF INVENTION: FAEL GENES AND THEIR USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```



```

APPLICATION NUMBER: US/08/888,998
FILING DATE: 07-JUL-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,603
FILING DATE: 26-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 12176-004300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 506 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..506
OTHER INFORMATION:
OTHER INFORMATION: /note="Amino acid sequence of PAEL
protein."
US-08-888-998-2

```

APPLICANT: JAMES, Douglas W.
 APPLICANT: LIM, Eda
 APPLICANT: KELLER, Janis
 APPLICANT: DOONER, Hugo K.
 TITLE OF INVENTION: FAEL GENES AND THEIR USES
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: Steuart Street Tower, One Market Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94105-1493
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/362,633
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/888,998
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bastian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 12176-004300
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 506 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..506
 OTHER INFORMATION: /note="Amino acid sequence of FAEL
 protein."
 US-09-362-633-2

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QY 388 SEOLLFPALLRRTSPDAKTTSTTSATKNGIKSSSSDLSPKPYDKLAEPHF 447
DB 354 SEKLEFPAFVAK-----KLRKIKHYVPDKRLAVDHF 368
QY 448 CFHAAKSVLEELÖKNLIGSEENMEASRMTLHREFGTSSSGIYELAYMEAKESVRGRD 507
DB 389 CHAGRAVAYDELEKNGLSPIDEASRSTLHREFGTSSSGIYELAYTEAKGRMKGNK 448
QY 508 WMOIAFGSGFKCNVYKAMRKVKKPTRRNPWDCINRYVPVL 550
DB 449 AMOIALGSGFKCNVAVVALRVN-KASANSPMQHCIDRIPVKI 490

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RESULT 10

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US-08-868-373-6
; Sequence 6, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868,373
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-868-373-6

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Query Match 41.1%; Score 1170.5; DB 4; Length 504;
Best Local Similarity 48.8%; Pred. No. 1.5e-113;
Matches 227; Conservative 75; Mismatches 126; Indels 37; Gaps 4;

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QY 95 DLATVIGFVGLVACVYFMSRPSRYLIDPACVPSDEHVKTEEFIELARKS----- 149
DB 66 NLQITSLILFLVFWLWILYMLTRKRPVYLVDSCYLPKSHKVSIGTLMGHARRAREGM 125
QY 150 ---GKPEETLGFKKRILOASGIDETVYPRSSSEITTMKGREASVITGALDEL 206
DB 126 CMKKESDHLVDFOEKILERSGLQOEYIIPGLOCPLOOGGASRRETEEVIGALDNL 185
QY 207 PEKRVKPKDVGVLVNCISIFNP7PSLAVINHYKMRGNILSYNLGMSGAGIITIDL 266
DB 186 FRNTGVKPDIGILVNVSSFTFN7PSLASMIYVKILRDNKISNLGMSGAGIYADV 245
QY 267 ARDMLGSPNSVAVVSTENAVGYWYVGSKSNVTPNCFRMSGSAVMSNRRDRFRAK 326
DB 246 AKGILQVHRTVAVVSTENITONLYTGKNSMLVTNCLFRVGAVALLSNRSRDRRAK 305
QY 327 YLEHYVTRKAAADDRSFVYOEDEOGFKGISRDLMVEGGEALKTITTLGPIVLP 386
DB 306 YELVHYVRIITGSDDSFEGATOEDEDDGIIIGVTLKKNLPMVARTLKINATIGPIVLP 365
QY 387 FSSQLLFPALLRRT-FSPAATSTTTSFSTSAKTNGIKSSSSDLSKRYIDYKLAPE 445
DB 366 LKEKLAFFITFVKKYFKPELRN-----YTPDFKLAPE 398
QY 446 HFCFHAASKVLEELÖKNLIGSEENMEASRMTLHREFGTSSSGIYELAYMEAKESVRG 505
DB 399 HFCIHAGGALIDELKKNKLSPLHVEASRMTLHREFGTSSSGIYELAYTEAKGRMKG 458
QY 506 DRVMOIAFGSGFKCNVYKAMRKVKKPTRRNPWDCINRYVPVL 550
DB 459 DRIWOIALGSGFKCNVAVVALRVN-KPSANSPEWDCMDRYPEI 502

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RESULT 11

```

US-08-888-998-4

```

```

; Sequence 4, Application US/08888998
; Patent No. 6124324
; GENERAL INFORMATION:
; APPLICANT: JAMES, Douglas W.
; APPLICANT: LIM, Eda
; APPLICANT: KELLER, Janis
; APPLICANT: DOONER, Hugo K.
; TITLE OF INVENTION: FAEL GENES AND THEIR USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Townsend and Townsend Kourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,998
; FILING DATE: 07-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,603
; FILING DATE: 26-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 12176-004300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..116
; OTHER INFORMATION: /note="partial amino acid sequence
; OTHER INFORMATION: of B. napus FAEL protein"
US-08-888-998-4

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Query Match 11.7%; Score 334; DB 3; Length 127;
Best Local Similarity 44.4%; Pred. No. 5e-27;
Matches 68; Conservative 22; Mismatches 37; Indels 26; Gaps 2;

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QY 334 RTHKAADDRSFVYOEDEOGFKGISRDLMVEGGEALKTITTLGPIVLPFSSQLLF 393
DB 1 RTHGADDKFRVCOGDDENGKIGVSLSKDITDVAGRTVKNVATLGPILPLSEKLLF 60
QY 394 FALLRRTSPAAKTTSTTSFSTSAKTNGIKSSSSDLSKPYIPDKLAHFCFHAAS 453
DB 61 FVTFM-----GKLPFDKIKHYVPDKLAIDHFCIH-RS 94
QY 454 KYVLEELÖKNLIGSEENMEASRMTLHREFGTSS 486
DB 95 RAVIDVLERNLAPIDVEASRSTLHREFGTSS 127

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RESULT 12

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US-09-362-633-4
; Sequence 4, Application US/09362633
; Patent No. 6184355
; GENERAL INFORMATION:
; APPLICANT: JAMES, Douglas W.
; APPLICANT: LIM, Eda

```

```

TITLE OF INVENTION: Plant Root Diseases
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Margaret A. Connor, Patent Advisor
STREET: 800 Buchanan St
CITY: Albany
STATE: CA
COUNTRY: USA
ZIP: 94710

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/994,035C
FILING DATE: 18-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Connor, Margaret A
REGISTRATION NUMBER: 30,043
REFERENCE/DOCKET NUMBER: 0009, 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 559 6067
TELEFAX: (510) 559 5736
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-994-035C-5

Query Match          6.0%; Score 169.5; DB 4; Length 349;
Best Local Similarity 21.8%; Pred. No. 4,4e-09;
Matches 90; Conservative 61; Mismatches 173; Indels 89; Gaps 15;

QY 130 KPS---DEKVTKEEFELARKSGKFEDELTGFKRRIQASGIGDETVPRIS-----180
    ||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 6 KPSLTFPHYKTIQQOMIDHLEQLHD-DHPRMALARKMIQNTQV-NERYLVLPIDELAVHT 63

QY 181 ---SSNITTMKEGREASTVIFGALDELFEKTRVXPXVG-VLVNCSIFNFTPSLNAV 237
    :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 64 GFTHSIVYEHRRARMSI---AARQAIENAGLTITDDIRMAVAVSCGF-MPISLTAHL 118

QY 238 INHYKRGNIISYNLGGMGCSAGIIAIDLARDMLQSNPSYAVVSTEMVGYNMYGSDK 297
    ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 119 INDGLKRTSYQLPITAOIGACVAGAAINRANFALSLSPNHALIYSLRSSL-CYQPDIT 177

QY 298 SM-VIPNCFPRMGCSAVMLSNRRDPFRHAKYRLHEIVYFKHADDRSFRSYQEBDEG 355
    :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 178 KLHAFISALTEGDAVASACVM-----RADDKA-----PG 205

QY 356 FKGLKISIDLMEVGEALKTNITITGLPLVLPSPSEQLLFPFALLKRTFSPAATSTTTSS 415
    :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 206 FK-----IAKTGSYFLPDPSEHYIVY-----DYKDSGFHF 234

QY 416 TSAFTKNGIKRSS---SDLKPYIPDYKIAFEHFCFPAASKVYLELOKNTGLSEENME 472
    ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 235 TLDRAYNMSIKDYAPAMEELNFETTNQCAQNDFFIFHTGGKIKIIDLVELYQLDLEPGRVA 294

QY 473 ASRMTLHRRFTSSSGIWELEYLAWEAKESVRRGRDVRWOITAFSGSGFKCNSVVRK 525
    ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 295 QSRDLSLEAGNIASY-VVEVDYLKRQFDGSGPANGATGMALAAFGPFTAEAVAKV 346

RESULT 14
US-09-395-861-5
: Sequence 5, Application US/09395861
: Patent No. 6447770
: GENERAL INFORMATION:
: APPLICANT: Raaijmakers, Jos M
: APPLICANT: Weller, David M

```

RESULT 15
US-08-494-907-12

[illegible]

Mon May 12 16:41:41 2003

us-09-905-657-2.rai

Page 9

Search completed: May 10, 2003, 23:54:33
Job time : 240 secs

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OM protein - protein search, using sw model

Run on: May 10, 2003, 22:53:14 ; Search time 1217 Seconds

(Without alignments)
93.119 Million cell updates/sec

Title: US-09-905-657-2

Perfect score: 2848

Sequence: 1 MGRSNGDLSTETVNRGIE.....KKPTRRNPWDCINRYPVL 550

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2844	99.9	550	10	091LE4
3	2841	99.8	550	10	091LE8
4	2840	99.7	550	10	091LE5
5	2605	91.5	508	10	091LE6
6	2324	81.6	535	10	08VWP9
7	2175.5	76.4	526	10	08S2K3
8	2005	70.4	389	10	091LE7
9	1820	63.9	352	10	091LE3
10	1784	62.6	351	10	091LE6
11	1569	55.1	516	10	091LE9
12	1494.5	52.5	509	10	048780
13	1492	52.4	512	10	09S1X1
14	1476.5	51.8	513	10	09FXZ8
15	1470.5	51.6	505	10	09FV67
16	1459	51.2	528	10	064485

17	1452	51.0	523	10	08VWX2	08VWX2 arabidopsis
18	1447	50.8	517	10	081658	081658 hemerocallis
19	1445	50.7	497	10	09XF43	09XF43 arabidopsis
20	1443	50.7	529	10	09F687	09F687 arabidopsis
21	1443	50.7	529	10	094CA1	094CA1 arabidopsis
22	1441	50.6	528	10	09MAM3	09MAM3 arabidopsis
23	1439	50.5	497	10	08VYJ5	08VYJ5 arabidopsis
24	1438	50.5	520	10	09ZTK3	09ZTK3 arabidopsis
25	1435	50.4	521	10	041301	041301 simmondsia
26	1402	49.2	487	10	065677	065677 arabidopsis
27	1397	49.1	503	10	08RXA6	08RXA6 tropaeolum
28	1372	48.2	492	10	09C6L5	09C6L5 arabidopsis
29	1316	46.2	598	10	094C75	094C75 oryza sativ
30	1215.5	42.7	532	10	09XEP1	09XEP1 sorghum bic
31	1213	42.6	451	10	09SUT9	09SUT9 arabidopsis
32	1205	42.3	506	10	08S3A2	08S3A2 brassica ol
33	1203	42.2	506	10	08S3A3	08S3A3 brassica na
34	1201	42.2	496	10	093XD5	093XD5 lequerella
35	1197.5	42.0	505	10	093J10	093J10 brassica na
36	1196.5	42.0	466	10	09ZU20	09ZU20 arabidopsis
37	1194	41.9	493	10	09SYZ0	09SYZ0 arabidopsis
38	1189	41.7	506	10	08S3A1	08S3A1 brassica ca
39	1188	41.7	506	10	093XF0	093XF0 brassica na
40	1186	41.6	506	10	038860	038860 arabidopsis
41	1181	41.5	506	10	08S3A0	08S3A0 brassica na
42	1180	41.4	506	10	023738	023738 brassica na
43	1170.5	41.1	476	10	09ZUK2	09ZUK2 arabidopsis
44	1154	40.5	621	10	09AXE6	09AXE6 dunaliella
45	1151.5	40.4	459	10	09SS39	09SS39 arabidopsis

ALIGNMENTS

RESULT 1

ID 064846 PRELIMINARY: PRT: 550 AA.
AC 064846:
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative beta-ketoacyl-CoA synthase (FIDDLEHEAD protein)
DE (AT2G26250/TID16.11).
GN TID16.11 OR FDH
GN Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RC Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RC Yephremov A., Wisman E., Huijser P., Huijser C., Wellesen K.,
RA Siedler H.;
RT "The FIDDLEHEAD gene, which mutation results in graft-like surface
RT tissue fusions in Arabidopsis thaliana, encodes an epidermis specific
RT condensing enzyme of lipid metabolism."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=CV. LANDSBERG ERRECTA;
RC MEDLINE=20122614; PubMed=10655527;
RA Pruitt R.E., Vielle-Calzada J.P., Ploense S.E., Grossniklaus U.,
RA Lohle S.J.;
RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
RT in Arabidopsis, encodes a putative lipid biosynthetic enzyme.";

Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).

[4] SEQUENCE FROM N.A.

RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.,
 RT "Full length cDNA of gene TID16.11/At2g26250 (GI:3075394).";
 RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]

RP SEQUENCE FROM N.A.

RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
 RA Davis R.W., Theologis A., Ecker J.R.,
 RT "Arabidopsis cDNA clones";
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC004484; AAC14526.1; -;
 DR EMBL: AJ010713; CA009311.1; -;
 DR EMBL: AF214490; AAF73973.1; -;
 DR EMBL: AF214489; AAF73973.1; JOINED.
 DR EMBL: AF337910; AAG60062.1; -;
 DR EMBL: AY039563; AAK62618.1; -;
 DR InterPro: IPR001099; N-C-synthase.
 DR Pfam: PF002797; Chal_stl_synthc.1.
 DR Prodom: PD000453; N-C-synthase; 2.
 SQ SEQUENCE 550 AA; 61961 MW; 5DB368601EDF174 CRC64;

Query Match 100.0%; Score 2848; DB 10; Length 550;
 Best Local Similarity 100.0%; Pred. No. 7.5e-228;
 Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSEODLLSTEIVNRGIEPSGNAGSPFVSVRRLPDLQSVNLYKYLGHYLYN 60
 DB 1 MGRSEODLLSTEIVNRGIEPSGNAGSPFVSVRRLPDLQSVNLYKYLGHYLYN 60

QY 61 HAVIATIPVLYVSAVGSLSREIWKKLMVDLAVIGFVGIVLTACVYFMSRPRS 120
 DB 61 HAVIATIPVLYVSAVGSLSREIWKKLMVDLAVIGFVGIVLTACVYFMSRPRS 120

QY 121 VYLIDFACYKPSDEHKYTKKEFIELARKSGKFEDETLGFKRRIQASGIGDETVPPRSIS 180
 DB 121 VYLIDFACYKPSDEHKYTKKEFIELARKSGKFEDETLGFKRRIQASGIGDETVPPRSIS 180

QY 181 SSEITITMKGREASVIFGALDELFEKTRVKPKDVGVLVNCISINPTPSLSAMYINH 240
 DB 181 SSEITITMKGREASVIFGALDELFEKTRVKPKDVGVLVNCISINPTPSLSAMYINH 240

QY 241 YKRGNTLSYNLGMCASAGITIAIDLRDLQSNPNSYAVVSTENGYVMYVGSDDSKSMV 300
 DB 241 YKRGNTLSYNLGMCASAGITIAIDLRDLQSNPNSYAVVSTENGYVMYVGSDDSKSMV 300

QY 301 IPNCFPMGCSAVMLNRRDPFRHAKYRLHIVTRHKAADDRFSRYOEDDQGRGLK 360
 DB 301 IPNCFPMGCSAVMLNRRDPFRHAKYRLHIVTRHKAADDRFSRYOEDDQGRGLK 360

QY 361 ISRDIMEVGEALKTNTITLGPLVLPFSQDLFFAALLRRTSPAKTSTTTSFSTSATY 420
 DB 361 ISRDIMEVGEALKTNTITLGPLVLPFSQDLFFAALLRRTSPAKTSTTTSFSTSATY 420

QY 421 KNGIKSSSDSKPIPYKLAFEHFCFHAASKVYLEELQKNLGLSEENMASRWTLLR 480
 DB 421 KNGIKSSSDSKPIPYKLAFEHFCFHAASKVYLEELQKNLGLSEENMASRWTLLR 480

QY 481 FGNITSSGIWELAYMEAKESYVRGDRVQIAFGSGFCNSYVMKAMRKVKKPTRNPNV 540
 DB 481 FGNITSSGIWELAYMEAKESYVRGDRVQIAFGSGFCNSYVMKAMRKVKKPTRNPNV 540

DB 481 FGNITSSGIWELAYMEAKESYVRGDRVQIAFGSGFCNSYVMKAMRKVKKPTRNPNV 540

QY 541 DCINNYPPVL 550
 DB 541 DCINNYPPVL 550

RESULT 2
 ID 09LE4
 AC 09LE4; PRELIMINARY; PRT; 550 AA.
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-JUN-2002 (TREMBlrel. 15, Last sequence update)
 DE Fiddlehead protein.
 GN FHL.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 NX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20122614; PubMed=10655527;
 RA Pruitt R.E., Velle-Calzada J.P., Ploense S.E., Grossniklaus U.,
 RA Lolle S.J.;
 RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 in Arabidopsis, encodes a putative lipid biosynthetic enzyme.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
 DR EMBL: AF214504; AAF73980.1; JOINED.
 DR EMBL: AF214503; AAF73980.1; JOINED.
 DR InterPro: IPR001099; N-C-synthase.
 DR Pfam: PF002797; Chal_stl_synthc.1.
 DR Prodom: PD000453; N-C-synthase; 2.
 SQ SEQUENCE 550 AA; 61960 MW; 53BD368601E75174 CRC64;

Query Match 99.9%; Score 2844; DB 10; Length 550;
 Best Local Similarity 99.8%; Pred. No. 1.6e-227;
 Matches 549; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSEODLLSTEIVNRGIEPSGNAGSPFVSVRRLPDLQSVNLYKYLGHYLYN 60
 DB 1 MGRSEODLLSTEIVNRGIEPSGNAGSPFVSVRRLPDLQSVNLYKYLGHYLYN 60

QY 61 HAVIATIPVLYVSAVGSLSREIWKKLMVDLAVIGFVGIVLTACVYFMSRPRS 120
 DB 61 HAVIATIPVLYVSAVGSLSREIWKKLMVDLAVIGFVGIVLTACVYFMSRPRS 120

QY 121 VYLIDFACYKPSDEHKYTKKEFIELARKSGKFEDETLGFKRRIQASGIGDETVPPRSIS 180
 DB 121 VYLIDFACYKPSDEHKYTKKEFIELARKSGKFEDETLGFKRRIQASGIGDETVPPRSIS 180

QY 181 SSEITITMKGREASVIFGALDELFEKTRVKPKDVGVLVNCISINPTPSLSAMYINH 240
 DB 181 SSEITITMKGREASVIFGALDELFEKTRVKPKDVGVLVNCISINPTPSLSAMYINH 240

QY 241 YKRGNTLSYNLGMCASAGITIAIDLRDLQSNPNSYAVVSTENGYVMYVGSDDSKSMV 300
 DB 241 YKRGNTLSYNLGMCASAGITIAIDLRDLQSNPNSYAVVSTENGYVMYVGSDDSKSMV 300

QY 301 IPNCFPMGCSAVMLNRRDPFRHAKYRLHIVTRHKAADDRFSRYOEDDQGRGLK 360
 DB 301 IPNCFPMGCSAVMLNRRDPFRHAKYRLHIVTRHKAADDRFSRYOEDDQGRGLK 360

QY 361 ISRDIMEVGEALKTNTITLGPLVLPFSQDLFFAALLRRTSPAKTSTTTSFSTSATY 420
 DB 361 ISRDIMEVGEALKTNTITLGPLVLPFSQDLFFAALLRRTSPAKTSTTTSFSTSATY 420

QY 421 KNGIKSSSDSKPIPYKLAFEHFCFHAASKVYLEELQKNLGLSEENMASRWTLLR 480
 DB 421 KNGIKSSSDSKPIPYKLAFEHFCFHAASKVYLEELQKNLGLSEENMASRWTLLR 480

QY 481 FGNITSSGIWELAYMEAKESYVRGDRVQIAFGSGFCNSYVMKAMRKVKKPTRNPNV 540
 DB 481 FGNITSSGIWELAYMEAKESYVRGDRVQIAFGSGFCNSYVMKAMRKVKKPTRNPNV 540

Db 481 FGNSSGIIWEIAYMEAKESVRGRDYMOLAFSGFCNCSYVKKARKYKPPRRNPWV 540
 QY 541 DCINRYPPVL 550
 Db 541 DCINRYPPVL 550

RESULT 3

Q9LLE8 ID Q9LLE8 PRELIMINARY; PRT; 550 AA.
 AC Q9LLE8;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Fiddlehead protein.
 GN FDI.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20122614; PubMed-10655527;
 RA Pruitt R.E., Vielle-Calzada J.P., Ploense S.E., Grossniklaus U.,
 RA Lohle S.J.;
 RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 in Arabidopsis, encodes a putative lipid biosynthetic enzyme";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
 DR EMBL; AF214496; AAF73976.1; -
 DR EMBL; AF214495; AAF73976.1; JOINED.
 DR InterPro: IPR001099; N-C_synthase.
 DR Pfam: PF02797; Chal_still_synthc; 1.
 DR ProDom: PD000453; N-C_synthase; 2.
 SQ SEQUENCE 550 AA; 62019 MM; 5DB336860310DEA4 CRC64;

Query Match 99.8%; Score 2841; DB 10; Length 550;
 Best Local Similarity 99.8%; Pred. No. 2.9e-227;
 Matches 549; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGRSNEODLSTELVNGIEPSGNAGSPFVSVRRRRLPDLQSVNLKYKLGHYLIN 60
 Db 1 MGRSNEODLSTELVNGIEPSGNAGSPFVSVRRRRLPDLQSVNLKYKLGHYLIN 60
 QY 61 HAVYIATIPVLVYFSAEVSLSREETIMKIMDYDLATVIGFGVFLTACVYFMSRPRS 120
 Db 61 HAVYIATIPVLVYFSAEVSLSREETIMKIMDYDLATVIGFGVFLTACVYFMSRPRS 120
 QY 121 VYLIDFACYRSDHKYTKKEEFILARKSGKFEDETLGFKRRIIQAASIGDETVPRIS 180
 Db 121 VYLIDFACYRSDHKYTKKEEFILARKSGKFEDETLGFKRRIIQAASIGDETVPRIS 180
 QY 181 SSENITTMKEGREASVYIFGALDELFEKTRVKPKDVGVLVNGSIFNPPTSLSAMYINH 240
 Db 181 SSENITTMKEGREASVYIFGALDELFEKTRVKPKDVGVLVNGSIFNPPTSLSAMYINH 240
 QY 241 YKMGNLTSTYNGMGCSAGIIDLARDMLQSNPNSTYAVVSTEMVGYNMYVGSDDSMV 300
 Db 241 YKMGNLTSTYNGMGCSAGIIDLARDMLQSNPNSTYAVVSTEMVGYNMYVGSDDSMV 300
 QY 301 IPNCFPMGCSAVMLSNRRDRFRRAKRYLREIVTRHKAADRSFRSYVQEDDEGFGGLK 360
 Db 301 IPNCFPMGCSAVMLSNRRDRFRRAKRYLREIVTRHKAADRSFRSYVQEDDEGFGGLK 360
 QY 361 ISRLMEVGEGALKTNTITTLGPIVLPFSEQLLFFAALLRRTFSPAATSTTSTSTATA 420
 Db 361 ISRLMEVGEGALKTNTITTLGPIVLPFSEQLLFFAALLRRTFSPAATSTTSTSTATA 420
 QY 421 KTNIGIKSSSDLSKPYIPDYKLAIEHFCFHAASKVYLEEIQKNGLSSEENMEASRMTLHR 480
 Db 421 KTNIGIKSSSDLSKPYIPDYKLAIEHFCFHAASKVYLEEIQKNGLSSEENMEASRMTLHR 480

QY 481 FGNSSGIIWEIAYMEAKESVRGRDYMOLAFSGFCNCSYVKKARKYKPPRRNPWV 540
 Db 481 FGNSSGIIWEIAYMEAKESVRGRDYMOLAFSGFCNCSYVKKARKYKPPRRNPWV 540
 QY 541 DCINRYPPVL 550
 Db 541 DCINRYPPVL 550

RESULT 4

Q9LLE5 ID Q9LLE5 PRELIMINARY; PRT; 550 AA.
 AC Q9LLE5;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Fiddlehead protein.
 GN FDI.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20122614; PubMed-10655527;
 RA Pruitt R.E., Vielle-Calzada J.P., Ploense S.E., Grossniklaus U.,
 RA Lohle S.J.;
 RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 in Arabidopsis, encodes a putative lipid biosynthetic enzyme";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
 DR EMBL; AF214502; AAF73979.1; -
 DR EMBL; AF214501; AAF73979.1; JOINED.
 DR InterPro: IPR001099; N-C_synthase.
 DR Pfam: PF02797; Chal_still_synthc; 1.
 DR ProDom: PD000453; N-C_synthase; 2.
 SQ SEQUENCE 550 AA; 62060 MM; FDB7283601B64672 CRC64;

Query Match 99.7%; Score 2840; DB 10; Length 550;
 Best Local Similarity 99.8%; Pred. No. 3.5e-227;
 Matches 549; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGRSNEODLSTELVNGIEPSGNAGSPFVSVRRRRLPDLQSVNLKYKLGHYLIN 60
 Db 1 MGRSNEODLSTELVNGIEPSGNAGSPFVSVRRRRLPDLQSVNLKYKLGHYLIN 60
 QY 61 HAVYIATIPVLVYFSAEVSLSREETIMKIMDYDLATVIGFGVFLTACVYFMSRPRS 120
 Db 61 HAVYIATIPVLVYFSAEVSLSREETIMKIMDYDLATVIGFGVFLTACVYFMSRPRS 120
 QY 121 VYLIDFACYRSDHKYTKKEEFILARKSGKFEDETLGFKRRIIQAASIGDETVPRIS 180
 Db 121 VYLIDFACYRSDHKYTKKEEFILARKSGKFEDETLGFKRRIIQAASIGDETVPRIS 180
 QY 181 SSENITTMKEGREASVYIFGALDELFEKTRVKPKDVGVLVNGSIFNPPTSLSAMYINH 240
 Db 181 SSENITTMKEGREASVYIFGALDELFEKTRVKPKDVGVLVNGSIFNPPTSLSAMYINH 240
 QY 241 YKMGNLTSTYNGMGCSAGIIDLARDMLQSNPNSTYAVVSTEMVGYNMYVGSDDSMV 300
 Db 241 YKMGNLTSTYNGMGCSAGIIDLARDMLQSNPNSTYAVVSTEMVGYNMYVGSDDSMV 300
 QY 301 IPNCFPMGCSAVMLSNRRDRFRRAKRYLREIVTRHKAADRSFRSYVQEDDEGFGGLK 360
 Db 301 IPNCFPMGCSAVMLSNRRDRFRRAKRYLREIVTRHKAADRSFRSYVQEDDEGFGGLK 360
 QY 361 ISRLMEVGEGALKTNTITTLGPIVLPFSEQLLFFAALLRRTFSPAATSTTSTSTATA 420
 Db 361 ISRLMEVGEGALKTNTITTLGPIVLPFSEQLLFFAALLRRTFSPAATSTTSTSTATA 420
 QY 421 KTNIGIKSSSDLSKPYIPDYKLAIEHFCFHAASKVYLEEIQKNGLSSEENMEASRMTLHR 480
 Db 421 KTNIGIKSSSDLSKPYIPDYKLAIEHFCFHAASKVYLEEIQKNGLSSEENMEASRMTLHR 480

QY 481 FGNSSSGIWEIAYMEAKESVRRGRDVMQIAGSSGFKCNSVYKAMRKVKKPPRRNPV 540
 DB 481 FGNSSSGIWEIAYMEAKESVRRGRDVMQIAGSSGFKCNSVYKAMRKVKKPPRRNPV 540
 QY 541 DCINRYVPPL 550
 DB 541 DCINRYVPPL 550

RESULT 5

Q9LE6 PRELIMINARY; PRT; 508 AA.
 ID Q9LE6
 AC Q9LE6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Fiddlehead protein.
 GN FDH.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20122614; PubMed-10655527;
 RA Pruitt R.E., Vielle-Calzada J.P., Ploense S.E., Grossniklaus U.,
 RA Lolle S.J.;
 RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 in Arabidopsis, encodes a putative lipid biosynthetic enzyme.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
 DR EMBL; AF214500; AAF73978.1;
 DR EMBL; AF214499; AAF73978.1; JOINED.
 DR InterPro: IPR001099; N-C-synthase.
 DR Pfam: PF02797; Chalcone synthase.
 DR Prodom: PD000453; N-C-synthase; 1.
 DR Prodom: PD000453; N-C-synthase; 2.
 SQ SEQUENCE 508 AA; 57043 MW; E034920567B0F96E CRC64;

Query Match 91.5%; Score 2605; DB 10; Length 508;
 Best Local Similarity 100.0%; Pred. No. 1e-207;
 Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSNEDELSTELVNRGIEPSGNAGSPTFSVRRRLPDLQSVNLKYLGYHYLIN 60
 DB 1 MGRSNEDELSTELVNRGIEPSGNAGSPTFSVRRRLPDLQSVNLKYLGYHYLIN 60
 QY 61 HAVYLAITPVLVFSAEVSLSREELMKLMVDLATVIGFVFLTACVYFMSRPS 120
 DB 61 HAVYLAITPVLVFSAEVSLSREELMKLMVDLATVIGFVFLTACVYFMSRPS 120
 QY 121 VYLDFACTYPSDEHKYTKKEEFTLARKSGKFEDETLGFKKRILOASGIDETVPSRS 180
 DB 121 VYLDFACTYPSDEHKYTKKEEFTLARKSGKFEDETLGFKKRILOASGIDETVPSRS 180
 QY 181 SSENITTMKREASIVIFGALDELFEKTRVPRKDVGLVYVNCSTINPTSLAMVINH 240
 DB 181 SSENITTMKREASIVIFGALDELFEKTRVPRKDVGLVYVNCSTINPTSLAMVINH 240
 QY 241 YKRGNITLSTNLGMCSSAGIITADLADMLQSNPNSTAVVSTENGYWYVGSOSM 300
 DB 241 YKRGNITLSTNLGMCSSAGIITADLADMLQSNPNSTAVVSTENGYWYVGSOSM 300
 QY 301 IPNCFRMCSSAVMLSNRRDRFRHAKYRLHEHYTRHKAADRSFRSVYOEDEGFGK 360
 DB 301 IPNCFRMCSSAVMLSNRRDRFRHAKYRLHEHYTRHKAADRSFRSVYOEDEGFGK 360
 QY 361 ISRDLMVEGALKNTITTLGPIVLPSEDLFFALLRRTSPAKTSTTSSTASATA 420
 DB 361 ISRDLMVEGALKNTITTLGPIVLPSEDLFFALLRRTSPAKTSTTSSTASATA 420
 QY 421 KNGIKSSSDLSKPYIPDYKLAHEHCFHAAKSVVLELOKNLGISENNMARSMTLHR 480
 DB 421 KNGIKSSSDLSKPYIPDYKLAHEHCFHAAKSVVLELOKNLGISENNMARSMTLHR 480

DB 421 KNGIKSSSDLSKPYIPDYKLAHEHCFHAAKSVVLELOKNLGISENNMARSMTLHR 480
 QY 481 FGNSSSGIWEIAYMEAKESVRRGRDVMQIAGSSGFKCNSVYKAMRKVKKPPRRNPV 540
 DB 481 FGNSSSGIWEIAYMEAKESVRRGRDVMQIAGSSGFKCNSVYKAMRKVKKPPRRNPV 540

RESULT 6

Q8VWP9 PRELIMINARY; PRT; 535 AA.
 ID Q8VWP9
 AC Q8VWP9;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Fiddlehead-like protein.
 GN FDH.
 OS Gossypium hirsutum (Upland cotton).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Gossypium.
 OX NCBI_Taxid=3635;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. XU-142; TISSUE-COTTON FIBER;
 RA Li C.-H., Zhu Y.-Q., Meng Y.-L., Wang J.-W., Xu K.-X., Zhang T.-Z.,
 RA Chen X.-Y.;
 RT "Isolation of Genes Preferentially Expressed in Cotton Fiber Cells by
 RT cDNA Array and RT-PCR."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY072823; AAL67993.1;
 DR InterPro: IPR001099; N-C-synthase.
 DR Pfam: PF02797; Chalcone synthase.
 DR Prodom: PD000453; N-C-synthase; 1.
 SQ SEQUENCE 535 AA; 61123 MW; D3E8A8CEA7E1A6DE CRC64;

Query Match 81.6%; Score 2324; DB 10; Length 535;
 Best Local Similarity 80.1%; Pred. No. 2.4e-184;
 Matches 438; Conservative 48; Mismatches 41; Indels 20; Gaps 2;

QY 5 NEODLSTELVNRGIEPSGNAGSPTFSVRRRLPDLQSVNLKYLGYHYLINHAY 64
 DB 4 NEODLSTELVNRGIEPSGNAGSPTFSVRRRLPDLQSVNLKYLGYHYLINHAY 63
 QY 65 LATIPVLVFSAEVSLREELMKLM---YDLATVIGFGVFLTACVYFMSRPSV 121
 DB 64 LATIPVLVFSAEVSLREELMKLMEDARYDLATVLSFAVFTVSVYFMSRPSI 123
 QY 122 YLIDFACTYPSDEHKYTKKEEFTLARKSGKFEDETLGFKKRILOASGIDETVPSRS 181
 DB 124 YLIDFACTYPSDEHKYTKKEEFTLARKSGKFEDETLGFKKRILOASGIDETVPSRS 183
 QY 182 SSENITTMKREASIVIFGALDELFEKTRVPRKDVGLVYVNCSTINPTSLAMVINH 241
 DB 184 KENCATMKREGLRSLASTVMPFALDELFEKTRIRPKDVGLVYVNCSTINPTSLAMVINH 243
 QY 242 KMGNITLSTNLGMCSSAGIITADLADMLQSNPNSTAVVSTENGYWYVGSOSM 301
 DB 244 KMGNITLSTNLGMCSSAGIITADLADMLQSNPNSTAVVSTENGYWYVGSOSM 303
 QY 302 PNCFFRMCSSAVMLSNRRDRFRHAKYRLHEHYTRHKAADRSFRSVYOEDEGFGK 361
 DB 304 PNCFFRMCSSAVMLSNRRDRFRHAKYRLHEHYTRHKAADRSFRSVYOEDEGFGK 363
 QY 362 SRDLMVEGALKNTITTLGPIVLPSEDLFFALLRRTSPAKTSTTSSTASATA 421
 DB 364 SKDLTEIGDALKNTITTLGPIVLPSEDLFFALLRRTSPAKTSTTSSTASATA 420
 QY 422 TNGIKSSSDLSKPYIPDYKLAHEHCFHAAKSVVLELOKNLGISENNMARSMTLHR 481
 DB 411 ----TSLSPSSKPYIPDYKLAHEHCFHAAKSVVLELOKNLGISENNMARSMTLHR 466
 QY 482 GNTSSSGIWEIAYMEAKESVRRGRDVMQIAGSSGFKCNSVYKAMRKVKKPPRRNPV 541
 DB 482 GNTSSSGIWEIAYMEAKESVRRGRDVMQIAGSSGFKCNSVYKAMRKVKKPPRRNPV 541

Db 467 GNTSSSIWELAYLEAKERVKRGDRIMQIAFGSGFKCNSVYVMSRMRYRKPDRPNMUD 526
 QY 542 CINTRYP 548
 Db 527 CIDRYP 533

RESULT 7

0852R3 PRELIMINARY; PRT; 526 AA.
 AC 0852R3;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Putative beta-ketoacyl-CoA synthase.
 GN APT.
 OS Antirrhinum majus (garden snapdragon).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Veroniceae; Antirrhinum.
 NCBI_TaxID=4151;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yephremov A., Eremova N., Heidmann I., Huijser P., Wellesen K.,
 RA Schwarz-Sommer Z., Saedler H.;
 RT "Epidermis-specific expression of FIDDLEHEAD-like genes in Arabidopsis
 RT and Antirrhinum";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ310739; CAC84082.D; -
 SO SEQUENCE 526 AA; 59277 MW; 43247EA83B257444 CRC64;

Query Match 76.4%; Score 2175.5; DB 10; Length 526;
 Best Local Similarity 74.8%; Pred. No. 5e-172;
 Matches 410; Conservative 60; Mismatches 47; Indels 31; Gaps 4;

QY 4 SNEODLSTELIYVNRGIEPSGPNAGSPTFSVRRRLPDLQSYNLKYYLGYHYLINNAV 63
 Db 2 ASEQMLSTELIYVNRGIE-----AGAMTFSVRRRLPDLQSYNLKYYLGYHYLINNGI 56
 QY 64 YLATIPVLYVLSAEVGSLSREIWKKLM-----YDLATVIGFGVYVLTACVYFMSRPR 119
 Db 57 YLATIPVLYVLSAEVGSLSREIWKKLM-----YDLATVIGFGVYVLTACVYFMSRPR 116
 QY 120 SYVILDFACYPSPDEHKTKKEEFIELARKSGKDEETLGFKRKRILOASIGDETVPRSI 179
 Db 117 SYVILDFACYPSPDLKTKKEEFIELARKSGKFTESSEFKRKRILOASIGDETVPRSI 176
 QY 180 SSENITTMKEGREGASTVIFGALDELFEKTRVYKPKDGVLYVNCISIFNPTPSISAMVIN 239
 Db 177 ASSENTATMKEGREASTVIFGALDELFEKTHIRPKDGVLYVNCISIFNPTPSISAMVIN 236
 QY 240 HYKMGNTLSYLGMGCSAGIATIDLDARMLQSNPNSAVVYSTEVMGYNNYVSDSKM 299
 Db 237 HYKMGNTLSYLGMGCSAGIATIDLDARMLQSNPNSAVVYSTEIVGNNYVSDSKM 296
 QY 300 VIPNCFPMGCSAVMLSNRRDRFRHAKYRLHEIVRTHKAADRSFRSVYQEDDQGFGLK 359
 Db 297 LIPNCFPMGCSAVMLSNRRDRYGRAKYRLHEIVRTHKGADRSFRSVYQEDDQGFGLK 356
 QY 360 KISRDLMEVGEALKTNTITTLGVLVLPFSEQLLFAALLRTFSPAKTSTTSTSTAT 419
 Db 357 KYSKDLVEIGEAIRKNTITTLGVLVLPFSEQLLFAALLRTFSPAKTSTTSTSTAT 408
 QY 420 AKTNGIKSSSSDLSPYIPDYKLAFEHCFHAAKSVYLELOKNGISLENNEASMTLH 479
 Db 409 -----SNPYIPDYKLAFEHCFHAAKSVYLELOKNGISLENNEASMTLH 455
 QY 480 REGNTSSGIWELAYLEAKESVRRGRDVMQIAFGSGFKCNSVYVMSRMRYRKPDRPNM 539
 Db 456 REGNTSSSIWELAYLEAKGIRKGRDVMQIAFGSGFKCNSVYVMSRMRYRKPDRPNM 514
 QY 540 VDCINRYP 547
 Db 527 CIDRYP 533

Db 515 VDCIDGYP 522

RESULT 8

09LE7 PRELIMINARY; PRT; 389 AA.
 AC 09LE7;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Fiddlehead protein.
 GN FDH.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eustoidae; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20122614; PubMed=10655527;
 RA Pruitt R.E., Vialle-Calzada J.P., Ploense S.E., Grossniklaus U.,
 RA Lollie S.J.;
 RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 RT in Arabidopsis, encodes a putative lipid biosynthetic enzyme.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
 DR EMBL; AF214498; AAF73977.1; JOINED.
 DR EMBL; AF214497; AAF73977.1; JOINED.
 DR InterPro; IPR001099; N-C_synthase.
 DR ProDom; PD000453; N-C_synthase; 1.
 SO SEQUENCE 389 AA; 43765 MW; 3F305FA5F8AE7523 CRC64;

Query Match 70.4%; Score 2005; DB 10; Length 389;
 Best Local Similarity 100.0%; Pred. No. 4.6e-158;
 Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSNEODLSTELIYVNRGIEPSGPNAGSPTFSVRRRLPDLQSYNLKYYLGYHYLIN 60
 Db 1 MGRSNEODLSTELIYVNRGIEPSGPNAGSPTFSVRRRLPDLQSYNLKYYLGYHYLIN 60
 QY 61 HAVYIATIPVLYVLSAEVGSLSREIWKKLMYDYLATVIGFGVYVLTACVYFMSRPRS 120
 Db 61 HAVYIATIPVLYVLSAEVGSLSREIWKKLMYDYLATVIGFGVYVLTACVYFMSRPRS 120
 QY 121 VYLIDPACPKPDEHKTKKEEFIELARKSGKDEETLGFKRKRILOASIGDETVPRSI 180
 Db 121 VYLIDPACPKPDEHKTKKEEFIELARKSGKDEETLGFKRKRILOASIGDETVPRSI 180
 QY 181 SSENITTMKEGREGASTVIFGALDELFEKTRVYKPKDGVLYVNCISIFNPTPSISAMVIN 240
 Db 181 SSENITTMKEGREGASTVIFGALDELFEKTRVYKPKDGVLYVNCISIFNPTPSISAMVIN 240
 QY 241 YKRGNTLSYLGMGCSAGIATIDLDARMLQSNPNSAVVYSTEVMGYNNYVSDSKM 300
 Db 241 YKRGNTLSYLGMGCSAGIATIDLDARMLQSNPNSAVVYSTEVMGYNNYVSDSKM 300
 QY 301 IPNCFPMGCSAVMLSNRRDRFRHAKYRLHEIVRTHKAADRSFRSVYQEDDQGFGLK 360
 Db 301 IPNCFPMGCSAVMLSNRRDRFRHAKYRLHEIVRTHKAADRSFRSVYQEDDQGFGLK 360
 QY 361 ISRDLMEVGEALKTNTITTLGVLVLPFSE 389
 Db 361 ISRDLMEVGEALKTNTITTLGVLVLPFSE 389
 RESULT 9
 09LE3 PRELIMINARY; PRT; 352 AA.
 AC 09LE3;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Fiddlehead protein.
 GN FDH.

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucotsids II; Brassicales; Brassicaceae; Arabidopsis.
 RN NCBL_TaxID=3702;
 RX MEDLINE-20122614; PubMed-10655527;
 RA Pruitt R.E., Velle-Calzada J.P., Ploense S.E., Grossniklaus U.,
 RA Lolle S.J.;
 RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 in Arabidopsis, encodes a putative lipid biosynthetic enzyme.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
 DR EMBL: AF214505; AAF73981.1; JOINED.
 DR InterPro: IPR001099; N-C-synthase.
 DR ProDom: PD000453; N-C-synthase; 1.
 SQ SEQUENCE 352 AA; 39793 MW; D311AB82396E286E CRC64;

Query Match 63.9%; Score 1820; DB 10; Length 352;
 Best Local Similarity 100.0%; Pred. No. 9.1e-143;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSNEODLLSTEIVNRGIEPSPGSPSPESVVRRLPDPFQSVNLYKLYGHYLN 60
 DB 1 MGRSNEODLLSTEIVNRGIEPSPGSPSPESVVRRLPDPFQSVNLYKLYGHYLN 60
 QY 61 HAVYATIPVLYVFSAEVGSLSREIWKRLMDYATVIGFGVFLVACVYFMSRPS 120
 DB 61 HAVYATIPVLYVFSAEVGSLSREIWKRLMDYATVIGFGVFLVACVYFMSRPS 120
 QY 121 VYLIDFACVPSDEHKVTEEFTELARKSGKFEDETLGFKRRLQASGIGDETVYPRSS 180
 DB 121 VYLIDFACVPSDEHKVTEEFTELARKSGKFEDETLGFKRRLQASGIGDETVYPRSS 180
 QY 181 SSENITTMKEGREASTVIFGALDELFEKTRVYKPKDVGVLVNCSTFNPPLSAMVINH 240
 DB 181 SSENITTMKEGREASTVIFGALDELFEKTRVYKPKDVGVLVNCSTFNPPLSAMVINH 240
 QY 241 YKRGNIISYNGMGCSAGIITAIIDARDMLQSNPSYAVVSTEMVGYNMYGSDKSNV 300
 DB 241 YKRGNIISYNGMGCSAGIITAIIDARDMLQSNPSYAVVSTEMVGYNMYGSDKSNV 300
 QY 301 IPNCFPRMGCSAVMLSNRRDRFRAKYLRLHIVTRHKAADRSFRSYQED 352
 DB 301 IPNCFPRMGCSAVMLSNRRDRFRAKYLRLHIVTRHKAADRSFRSYQED 352

RESULT 10

Q9LNDX6 PRELIMINARY; PRT; 351 AA.
 AC Q9LNDX6;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Fiddlehead protein.
 GN FHL.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucotsids II; Brassicales; Brassicaceae; Arabidopsis.
 RN NCBL_TaxID=3702;
 RX MEDLINE-20122614; PubMed-10655527;
 RA Pruitt R.E., Velle-Calzada J.P., Ploense S.E., Grossniklaus U.,
 RA Lolle S.J.;
 RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 in Arabidopsis, encodes a putative lipid biosynthetic enzyme.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
 DR EMBL: AF214493; AAF73975.1; JOINED.
 DR EMBL: AF214492; AAF73974.1; -

DR EMBL: AF214491; AAF73974.1; JOINED.
 DR InterPro: IPR001099; N-C-synthase.
 DR ProDom: PD000453; N-C-synthase; 1.
 SQ SEQUENCE 351 AA; 39810 MW; 41F0CD279D141BC8 CRC64;

Query Match 62.6%; Score 1784; DB 10; Length 351;
 Best Local Similarity 100.0%; Pred. No. 8.9e-140;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSNEODLLSTEIVNRGIEPSPGSPSPESVVRRLPDPFQSVNLYKLYGHYLN 60
 DB 1 MGRSNEODLLSTEIVNRGIEPSPGSPSPESVVRRLPDPFQSVNLYKLYGHYLN 60
 QY 61 HAVYATIPVLYVFSAEVGSLSREIWKRLMDYATVIGFGVFLVACVYFMSRPS 120
 DB 61 HAVYATIPVLYVFSAEVGSLSREIWKRLMDYATVIGFGVFLVACVYFMSRPS 120
 QY 121 VYLIDFACVPSDEHKVTEEFTELARKSGKFEDETLGFKRRLQASGIGDETVYPRSS 180
 DB 121 VYLIDFACVPSDEHKVTEEFTELARKSGKFEDETLGFKRRLQASGIGDETVYPRSS 180
 QY 181 SSENITTMKEGREASTVIFGALDELFEKTRVYKPKDVGVLVNCSTFNPPLSAMVINH 240
 DB 181 SSENITTMKEGREASTVIFGALDELFEKTRVYKPKDVGVLVNCSTFNPPLSAMVINH 240
 QY 241 YKRGNIISYNGMGCSAGIITAIIDARDMLQSNPSYAVVSTEMVGYNMYGSDKSNV 300
 DB 241 YKRGNIISYNGMGCSAGIITAIIDARDMLQSNPSYAVVSTEMVGYNMYGSDKSNV 300
 QY 301 IPNCFPRMGCSAVMLSNRRDRFRAKYLRLHIVTRHKAADRSFR 345
 DB 301 IPNCFPRMGCSAVMLSNRRDRFRAKYLRLHIVTRHKAADRSFR 345

RESULT 11

Q9LND49 PRELIMINARY; PRT; 516 AA.
 AC Q9LND49;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE F18014.21.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucotsids II; Brassicales; Brassicaceae; Arabidopsis.
 RN NCBL_TaxID=3702;
 RX MEDLINE-20122614; PubMed-10655527;
 RA Pruitt R.E., Velle-Calzada J.P., Ploense S.E., Grossniklaus U.,
 RA Lolle S.J.;
 RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 in Arabidopsis, encodes a putative lipid biosynthetic enzyme.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
 DR EMBL: AF214493; AAF73975.1; JOINED.
 DR ProDom: PD000453; N-C-synthase; 1.
 SQ SEQUENCE 516 AA; 57842 MW; 3EDD488EE755C367 CRC64;

Query Match 55.1%; Score 1569; DB 10; Length 516;
 Best Local Similarity 56.5%; Pred. No. 1.2e-121;
 Matches 300; Conservative 82; Mismatches 117; Indels 32; Gaps 5;

QY 23 GPNAGSPFESVVRRLPDPFQSVNLYKLYGHYLNHAVYATIPVLYVFSAEVGS 82
 DB 13 GGDGDSVGVQIRGTRALPDLQSVNLYKLYGHYLNILTLCLFP-LAVYIVSEASON 71

[illegible]

RESULT 12			
ID	048780	PRELIMINARY;	PRT;
AC	048780;		509 AA.
DT	01-JUN-1998 (TREMBLrel. 06, Created)		
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Putative beta-ketoacyl-CoA synthase.		
GN	ATG26640.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Brassicaceae;		
OC	Eurosid II; Brassicales; Brassicaceae; Arabidopsis.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV. COLUMBIA.		
RX	MEDLINE-20083487; PubMed-10617197;		
RA	Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,		
RA	Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,		
RA	Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.		
RA	Crozin L.A., Shen M., Vanaken S.E., Unayam L., Tallon L.J., Gill J.E.		
RA	Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,		
RA	Copenhaver G.P., Preuss D., Nierman J.C., White O., Eisen J.A.,		
RA	Salzberg S.L., Fraser C.M., Venter J.C.;		
RT	"Sequence and analysis of chromosome 2 of the plant Arabidopsis		
RT	thaliana.";		
RL	Nature 402:761-768(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV. COLUMBIA;		
RA	Lin X.;		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AC003105; AB95298.1; -;		
DR	InterPro; IPR001099; N-C_synthase.		
DR	InterPro; IPR001848; Ribosomal_S10.		
DR	Pfam; PF02797; Chal_stil_synthc; 1.		
DR	ProDom; PD000453; N-C_synthase; 2.		
DR	PROSITE; PS00361; RIBOSOMAL_S10; UNKNOWN_1.		
QO	SEQUENCE 509 AA; 57814 MW; DB922BC82B33662F CRC64;		

Query Match	Similarity	52.5%	Score 1494.5	DB 10	Length 509
Best Local Match	54.8%	Pred. No. 1.7e-115			
Batches 283	Conservative	88	Mismatches 112	Indels 33	Gaps 5
Oy	37	RRLPFILOSVMNLKYKGLGAYHYLLINAVVLAATIPVLVLFSAEVSGLSREETIMKLMND--	93		
Db	15	RLPLDPFKRSVYKLVYKGLGAYHYLLINAVVLAATIPVLVLFSAEVSGLSREETIMKLMND--	72		
Oy	94	YDLATVIFPGFYVITACVYFMSRPSRYLLIDFACVPSDEHKVYKEEFIELARKSGKFD	153		
Db	73	YNLSVYVVCMSMLVFLMYFLMYFEMTRRPPYLVVFCFCKDESKCYTKLTFMRSKLTGSGFT	132		
Oy	154	EEITGFKRRIIOASGISGETVYVPSRISSESENTITMKEGREASVYIPGALDELFEKTRVK	213		
Db	133	ENLEFORKLIIORSGLGISTYLPPEAVLVNPPNCPCKEARKLEAYVFGAIDELAKTIVN	192		
Oy	214	PKDVGVLVNCSSIFNPPTSLSAMVINHYKMRGNILSYNLGNGCSAGIATIDALMDLOS	273		
Db	193	PRDIIILLVNCSSIFNPPTSLSAMVINHYKMRGNILSYNLGNGCSAGIATIDALMDLOS	252		
Oy	274	NPNSSAVVSTDEMGVYNTVGSDDKSMVLPNCFPRGCSAVALMSNRDRFRAKTYLEIV	333		
Db	253	IPNTAAVYISMENTILNMYFGNDRSKLVSNCLFPRGGAAILLSNRKMRORSKVELVPTV	312		
Oy	334	RTHKAAADRSPFSVYQDEEDGFKLTSRDLMEVGGELKNTINTTLGVLVFPSEQLLF	393		
Db	313	RTHKAAADKRCGCGITQEDDSASKIGVITYSKELMAVAGDALKTINTTLGVLVFPSEQLLF	372		
Oy	394	FAALL-RRTEFSPAATSTTTSSTSTSAATKATNGIKSSSDLSKPYTIDYKLAIEHFCFHA	452		
Db	373	FATLVGRKLFKFKKI-----KPYIDPKLAFEHFCHIA	405		
Oy	453	SKVYVEELQKNIIGSEENMEASRMVLHFRGNTSSGIVETAYLAAMAKSVRGDPVQIA	512		
Db	406	GGAVIDELEKNIKLTETHEMEBPSRMVLHFRGNTSSSGLIWEYLAISPAKRIKKDRIQWIA	465		
Oy	513	FGSGFCNCSVYKAKRKVKKPTRRNPWDJCINRPV	548		
Db	466	FGSGFCNCSVYKAVRSVNPVKKRPMDIEHFV	501		
RESULT 13					
Q9SIX1					
ID	Q9SIX1	PRELIMINARY:	PRT:	512 AA.	
AC	Q9SIX1				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Putative beta-ketoacyl-CoA synthase.				
GN	ATG16280.				
OS	Arabidopsis thaliana (Mouse-ear cress).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.				
OX	NCBI_TaxID=3702;				
RN	[1]				
RA	SEQUENCE FROM N.A.				
RC	STRAIN=CV. COLOMBIA.				
RA	MEDLINE=20083487; PubMed=10617197;				
RA	Lih X., Kaul S.P., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,				
RA	Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldlyum T.V.,				
RA	Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,				
RA	Cronin L.A., Shea M., Vankken S.E., Umayam L., Taiton L.J., Gill J.E.,				
RA	Adams M.D., Carrera A.J., Cressy T.H., Goodman H.M., Somerville C.R.,				
RA	Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,				
RA	Salzberg S.L., Fraser C.M., Venter J.C.;				
RT	"Sequence and analysis of chromosome 2 of the plant Arabidopsis				
RT	thaliana.";				
RL	Nature 402:761-768(1999).				
RM	[2]				
RC	SEQUENCE FROM N.A.				
RC	STRAIN=CV. COLOMBIA.				

ID	RESULT 14	
09FXZ8		
09FXZ8	PRELIMINARY;	PRT; 513 AA.
09FXZ8;		
01-MAR-2001	(TREMBLrel. 16, Created)	
01-MAR-2001	(TREMBLrel. 16, last sequence update)	
01-JUN-2002	(TREMBLrel. 21, last annotation update)	
DE	Purified fatty acid elongase.	
FAEZ		
zea mays (Maize).		
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
CC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade	
CC	Panicoidae; Andropogoneae; zea.	
CC	NCBI_TaxID=4577;	
NN	[1]	
NN	SEQUENCE FROM N.A.	
RP	MEDLINE=21116804; PubMed=11171156;	
XX	Schreiber L., Skrabbs M., Hartmann K., Becker D., Cassagne C.,	
VA	Leessie R.;	
VA	"Biochemical and molecular characterisation of corn (Zea mays L.) root	
TT	elongases.";	
TT	Biochem. Soc. Trans. 28:647-649(2000).	
TT	EMBL; AJ292770; CAC01441.1;	
TT	InterPro; IPR0010109; N-C_synthase.	

RESULT 15	Q9FW67	PRELIMINARY;	PRT;	505 AA.
ID	Q9FW67			
AC	Q9FW67;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DD	01-MAR-2001 (TREMBLrel. 16, last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)			
DE	Fatty acid elongase 1-like protein.			
OS	Limnanthes douglasii (Douglas's meadowfoam).			
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophytes I; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eucots II; Brassicales; Limnanthaceae; Limnantes.			
NCBI	NCBI_TxId-28973;			
RNA	[1]			
SEQUENCE FROM N.A.				
RRP	TISSUE=DEVELOPING SEED;			
RC	MEDLINE=20438218; PubMed=10982439;			
RR	Cañon E.B., Marillia E.F., Stecca K.L., Hall S.E., Taylor D.C.,			
RA	Klinsky A.J.;			
RT	"Production of fatty acid components of meadowfoam oil in somatic			
RT	soybean embryos.";			
RL	Plant Physiol. 124:243-252(2000).			
EMBL	EMBL; AF247134; AAC28600.1;			
OR	InterPro: IPR001099; N-C-synthase.			
OR	Pfam: PF02797; Chal_stl_synthc; 1.			
OR	ProDom: PD000453; N-C-synthase; 1.			
OR	SEQUENCE 505 AA; 56549 MW; EFCA1BAD807B0A56 CRC64;			

[illegible]

Search completed: May 10, 2003, 23:40:20
Job time : 1221 secs

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OM protein - protein search, using sw model

Run on: May 10, 2003, 23:50:32 ; Search time 613 Seconds

(without alignments)
82.568 Million cell updates/sec

Title: US-09-905-657-2

Perfect score: 2848
Sequence: 1 MGRSNEQDLSTEIVNRGIE.....KKPTRRNPWVCINRYPVPL 550

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2848	100.0	550	10	US-09-905-657-2 Sequence 2, Appl 1
2	2845	99.9	550	10	US-09-883-797-8 Sequence 8, Appl 1
3	1569	55.1	516	10	US-09-883-797-14 Sequence 14, Appl 1
4	1493	52.4	537	10	US-09-883-797-10 Sequence 10, Appl 1
5	1446.5	50.8	500	10	US-09-883-797-12 Sequence 12, Appl 1
6	1445	50.7	497	10	US-09-892-325-4 Sequence 4, Appl 1
7	1438	50.5	520	10	US-09-883-797-2 Sequence 2, Appl 1
8	1200	42.1	506	10	US-09-877-476-42 Sequence 42, Appl 1
9	1197.5	42.0	505	10	US-09-877-476-6 Sequence 6, Appl 1
10	1194	41.9	493	10	US-09-883-797-4 Sequence 4, Appl 1
11	1193	41.9	506	10	US-09-877-476-32 Sequence 32, Appl 1
12	1190	41.8	506	10	US-09-877-476-38 Sequence 38, Appl 1
13	1190	41.8	506	10	US-09-877-476-40 Sequence 40, Appl 1
14	1187	41.7	506	10	US-09-877-476-34 Sequence 34, Appl 1
15	1186	41.6	506	10	US-09-877-476-2 Sequence 2, Appl 1
16	1186	41.6	506	10	US-09-877-476-16 Sequence 16, Appl 1
17	1183	41.5	506	10	US-09-877-476-22 Sequence 22, Appl 1
18	1183	41.5	506	10	US-09-877-476-26 Sequence 26, Appl 1
19	1183	41.5	506	10	US-09-877-476-36 Sequence 36, Appl 1

20	1182	41.5	506	10	US-09-877-476-24 Sequence 24, Appl 1
21	1181	41.5	506	10	US-09-877-476-20 Sequence 20, Appl 1
22	1180	41.4	506	10	US-09-877-476-4 Sequence 4, Appl 1
23	1179	41.4	506	10	US-09-877-476-28 Sequence 28, Appl 1
24	1176	41.3	506	10	US-09-877-476-14 Sequence 14, Appl 1
25	1175	41.3	506	10	US-09-877-476-8 Sequence 8, Appl 1
26	1174	41.2	506	10	US-09-877-476-12 Sequence 12, Appl 1
27	1173	41.2	506	10	US-09-877-476-30 Sequence 30, Appl 1
28	1172.5	41.2	505	10	US-09-877-476-18 Sequence 18, Appl 1
29	1170.5	41.1	504	10	US-09-877-476-6 Sequence 6, Appl 1
30	1165.5	40.9	505	10	US-09-877-476-10 Sequence 10, Appl 1
31	156	5.5	351	9	US-09-829-378-5 Sequence 5, Appl 1
32	148.5	5.2	83	10	US-09-903-456-8 Sequence 8, Appl 1
33	145	5.1	317	10	US-09-815-242-14037 Sequence 14037, A
34	141	5.0	317	10	US-09-815-242-10124 Sequence 10124, A
35	131.5	4.6	313	10	US-09-815-242-12528 Sequence 12528, A
36	127.5	4.5	360	9	US-09-829-378-3 Sequence 3, Appl 1
37	125.5	4.4	394	10	US-09-837-654-1 Sequence 1, Appl 1
38	125.5	4.4	394	10	US-09-837-554-1 Sequence 1, Appl 1
39	122	4.3	331	10	US-09-815-242-11484 Sequence 11484, A
40	122	4.3	360	9	US-09-829-378-4 Sequence 4, Appl 1
41	117	4.1	316	10	US-09-815-242-10976 Sequence 10976, A
42	115.5	4.1	744	9	US-10-270-875-12 Sequence 12, Appl 1
43	115.5	4.1	744	9	US-10-270-878-12 Sequence 12, Appl 1
44	107	3.8	412	9	US-09-829-378-2 Sequence 2, Appl 1
45	102.5	3.6	360	9	US-09-829-378-6 Sequence 6, Appl 1

ALIGNMENTS

RESULT 1

US-09-905-657-2
Sequence 2, Application US/09905657
Patent No. US20020038471A1
GENERAL INFORMATION:
APPLICANT: BAYER AG
TITLE OF INVENTION: Use of VICEFAR for identifying herbicidally
FILE REFERENCE: Le A 34 730
CURRENT APPLICATION NUMBER: US/09/905,657
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 550
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-905-657-2

Query Match	100.0%	Score 2848	DB 10	Length 550
Best Local Similarity	100.0%	Pred. No. 3.3e-236		
Matches 550	Conservative 0	Mismatches 0	Indels 0	Gaps 0
OY	1	MGRSNEQDLSTEIVNRGIEPSGPNAGSPTEFSVRRRLPDFLOSYNLKYKLGHYLIN	60	
DB	1	MGRSNEQDLSTEIVNRGIEPSGPNAGSPTEFSVRRRLPDFLOSYNLKYKLGHYLIN	60	
OY	61	HAVYATATPVLVLFVFAEYSGLSREIEIMKLMYDYLATVIGFVFLTACVYFMSRPS	120	
DB	61	HAVYATATPVLVLFVFAEYSGLSREIEIMKLMYDYLATVIGFVFLTACVYFMSRPS	120	
OY	121	VYLIDPACRPPSEHNTVEEFTELARKSGKPEDETLGKRRILQASGIGDEYVRSIS	180	
DB	121	VYLIDPACRPPSEHNTVEEFTELARKSGKPEDETLGKRRILQASGIGDEYVRSIS	180	
OY	181	SEENITMKEGREASTVFGALDELFEKTRVPRKGVYLVNCSIFNPTPSANVINH	240	
DB	181	SEENITMKEGREASTVFGALDELFEKTRVPRKGVYLVNCSIFNPTPSANVINH	240	
OY	241	YKMRGNIISYNLGCMGCSAGIATIDARDMLQSNPNSYAVVSTENVGYNMVYGSQSMV	300	
DB	241	YKMRGNIISYNLGCMGCSAGIATIDARDMLQSNPNSYAVVSTENVGYNMVYGSQSMV	300	

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QY 301 IPNCFRMCSSAYMLSNRRDPRHAKYRLHEIVRTHKAADRSFRSYOEDEGGFGK 360
Db 301 IPNCFRMCSSAYMLSNRRDPRHAKYRLHEIVRTHKAADRSFRSYOEDEGGFGK 360
QY 361 ISDLMVEVGEALKTNTTTLGPIVLPSEQLLFPALLRTPSPAATSTTTSFSTATA 420
Db 361 ISDLMVEVGEALKTNTTTLGPIVLPSEQLLFPALLRTPSPAATSTTTSFSTATA 420
QY 421 KTGKIKSSSSDLSPYIPDKLAFEHFCFHAASKVYLEEOKNLGISEENMEASRMTLHR 480
Db 421 KTGKIKSSSSDLSPYIPDKLAFEHFCFHAASKVYLEEOKNLGISEENMEASRMTLHR 480
QY 481 FGTSSSGIWEELAYEAKESVRRGDRVQWQIAFGSGFKNSVYWKAMRYKKPTRNPNW 540
Db 481 FGTSSSGIWEELAYEAKESVRRGDRVQWQIAFGSGFKNSVYWKAMRYKKPTRNPNW 540
QY 541 DCINRYPVPL 550
Db 541 DCINRYPVPL 550

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RESULT 2
US-09-883-797-8
; Sequence 8, Application US/09883797
; Patent No. US20020066123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemmiller, Martha A.
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-883-797-8

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Query Match 99.98; Score 2845; DB 10; Length 550;
Best Local Similarity 99.88; Pred. No. 6.4e-256;
Matches 549; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGRSNEODLLSTETIVNRGIEPSPGPNAGSPFVSRRRLPDLQSVNLKYKLGHYHLIN 60
Db 1 MGRSNEODLLSTETIVNRGIEPSPGPNAGSPFVSRRRLPDLQSVNLKYKLGHYHLIN 60
QY 61 HAYLATIPLVLYFSAEVGSLSREETIMKLMYDLATVIGFVFLTACVYFMSRPRS 120
Db 61 HAYLATIPLVLYFSAEVGSLSREETIMKLMYDLATVIGFVFLTACVYFMSRPRS 120
QY 121 VYLIDFACYPSDEHKYTKKEETELAKRSKGFDEETGFFKRILQASGIDETVPPRSIS 180
Db 121 VYLIDFACYPSDEHKYTKKEETELAKRSKGFDEETGFFKRILQASGIDETVPPRSIS 180
QY 181 SSENITTMKREGEASTVIGALDELFEKTRVPRKDVGVVNCSTINPTPSISAMVINH 240
Db 181 SSENITTMKREGEASTVIGALDELFEKTRVPRKDVGVVNCSTINPTPSISAMVINH 240
QY 241 YKRGITLSYNLGMCSSAGIIAIDLARMLQSNPNSTAVVSTEMVGYWYGSOKSMV 300
Db 241 YKRGITLSYNLGMCSSAGIIAIDLARMLQSNPNSTAVVSTEMVGYWYGSOKSMV 300
QY 301 IPNCFRMCSSAYMLSNRRDPRHAKYRLHEIVRTHKAADRSFRSYOEDEGGFGK 360
Db 301 IPNCFRMCSSAYMLSNRRDPRHAKYRLHEIVRTHKAADRSFRSYOEDEGGFGK 360
QY 361 ISDLMVEVGEALKTNTTTLGPIVLPSEQLLFPALLRTPSPAATSTTTSFSTATA 420

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Db 361 ISDLMVEVGEALKTNTTTLGPIVLPSEQLLFPALLRTPSPAATSTTTSFSTATA 420
QY 421 KTGKIKSSSSDLSPYIPDKLAFEHFCFHAASKVYLEEOKNLGISEENMEASRMTLHR 480
Db 421 KTGKIKSSSSDLSPYIPDKLAFEHFCFHAASKVYLEEOKNLGISEENMEASRMTLHR 480
QY 481 FGTSSSGIWEELAYEAKESVRRGDRVQWQIAFGSGFKNSVYWKAMRYKKPTRNPNW 540
Db 481 FGTSSSGIWEELAYEAKESVRRGDRVQWQIAFGSGFKNSVYWKAMRYKKPTRNPNW 540
QY 541 DCINRYPVPL 550
Db 541 DCINRYPVPL 550

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RESULT 3
US-09-883-797-14
; Sequence 14, Application US/09883797
; Patent No. US20020066123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemmiller, Martha A.
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-883-797-14

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Query Match 55.18; Score 1569; DB 10; Length 516;
Best Local Similarity 56.58; Pred. No. 2.6e-137;
Matches 300; Conservative 82; Mismatches 117; Indels 32; Gaps 5;
QY 23 GPNAGSPFVSRRRLPDLQSVNLKYKLGHYHLINHAAYLATIPLVLYFSAEVGS 82
Db 23 GPNAGSPFVSRRRLPDLQSVNLKYKLGHYHLINHAAYLATIPLVLYFSAEVGS 82
QY 13 GGGGDSVGVQIRQIRMLPDLQSVNLKYKLGHYHLINLTLLCLFP-LAVIVISVASQM 71
Db 13 GGGGDSVGVQIRQIRMLPDLQSVNLKYKLGHYHLINLTLLCLFP-LAVIVISVASQM 71
QY 83 SREIETKRLW--DYDLATVIGFVFLTACVYFMSRPRSIVLIDFACYPSDEHKYTK 139
Db 83 SREIETKRLW--DYDLATVIGFVFLTACVYFMSRPRSIVLIDFACYPSDEHKYTK 139
QY 140 EEFIELARKSGKDEDETLGFEKRILOASGIDETVPPRSISSSENITTMKREGEASTVI 199
Db 140 EEFIELARKSGKDEDETLGFEKRILOASGIDETVPPRSISSSENITTMKREGEASTVI 199
QY 191 FGALDNLFPANTINVKPRKIGILVNCSTLFPNTPPSISAMVINHYKRGITLSYNLGMCSSA 250
Db 191 FGALDNLFPANTINVKPRKIGILVNCSTLFPNTPPSISAMVINHYKRGITLSYNLGMCSSA 250
QY 250 GIATIDLARMLQSNPNSTAVVSTEMVGYWYGSOKSMVIPNCFRMCSSAYMLSNRR 319
Db 250 GIATIDLARMLQSNPNSTAVVSTEMVGYWYGSOKSMVIPNCFRMCSSAYMLSNRR 319
QY 319 RDRRSKRYRLVHYRTHRGADDAFCRCVYOEODTGTGVSLSKDLAINGETLKTNTT 370
Db 319 RDRRSKRYRLVHYRTHRGADDAFCRCVYOEODTGTGVSLSKDLAINGETLKTNTT 370
QY 371 LGPIVLPSEQLLFPALLRTPSPAATSTTTSFSTATAKNGIKSSSDLSKPYIPD 439
Db 371 LGPIVLPSEQLLFPALLRTPSPAATSTTTSFSTATAKNGIKSSSDLSKPYIPD 439
QY 440 YKLAFFHFCFHAASKVYLEEOKNLGISEENMEASRMTLHRFGNTSSSGIWEELAYEAK 499
Db 440 YKLAFFHFCFHAASKVYLEEOKNLGISEENMEASRMTLHRFGNTSSSGIWEELAYEAK 499

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OY 500 ESVRGDRVMOIARSGFKNSVYWKAMRKVKPTRRNNPWDCINRYVPL 550
Db 465 GRMRGRNVMOIARSGFKNSAIWEALRHV-KPSNNSPWEDCIDKJPVTL 514

RESULT 4

US-09-883-797-10
; Sequence 10, Application US/09883797
; Patent No. US2002006123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 537
; TYPE: PR1
; ORGANISM: Arabidopsis thaliana
US-09-883-797-10

Query Match 52.4%; Score 1493; DB 10; Length 537;
Best Local Similarity 52.6%; Pred. No. 3.3e-130;
Matches 287; Conservative 103; Mismatches 116; Indels 40; Gaps 9;

OY 12 TEIYNRGIEPSGPNAGSPTSVR---RRRLPDFLOSVMKLYKLGHYHLYINHAVALYAT 67
Db 23 SEAEANAE--VNGS--VOIRTEENERRKLPHFLOSVMKLYKLGHYHLYITHFKLCL 78
OY 68 IPVLVLSAEVSLRSREIKKTL--DYDLAVYGFVGLTACVYFMSRPSRYLI 124
Db 79 VP-LMAVLVETISRLTDDLT-QIWLHQYLVAFIFLSALATIGSTVYIMSRPSRYLV 136
OY 125 DFACYKPSDEHKTKEEFIELARKSGDETLGFKRRILOASGIDETVYPRSSSEN 184
Db 137 DYSCLPESLOVYKQFMDSKLIEDENESSLEFQRKILRSGLGETVYPEALHCP 196
OY 185 ITTKEGREASVYIFGALDELFEKTRVAKPDVGLVYVNCISFNPPLSAMVINHYMR 244
Db 197 RPTMAARESEOVYMFGLDKLFENTKINPRDIGLVVNCISLFPPLSAMVYKYL 256
OY 245 GNLSYNLGSGSAGIATIDLARDMLQSNYSYAVVSTWGVGMVYVGSDDKSVIPNC 304
Db 257 GNVSPNLGSGSAGVATIDLADMLQVHNRTAVVSTENITONMIFGKAKMLINC 316
OY 305 FFMGCSAVMLSNRRDFRRAKRYLEHIVTHKAADRSFVSVOEEDOGFKLISRD 364
Db 317 LFRVGSAILLSNKGKDRRSKYLIVHTVTHKGAVEKAFVYQOEDDNGKTVGLSKD 376
OY 365 LMEVGELAKNTITLGPVLPFSEQLFPAALLRRTSPAAKTSTTTSFSTATAKING 424
Db 377 LMAIAGEELKANTITLGLVLPISBQILFMTLVTK----- 412
OY 425 IKSSSDLSKRPIDYKLAFFHCFHAAKSVYLELOKNLGLSEEMEASRMTLHFRGNT 484
Db 413 -KLENSKL-KRYPDFKLAFFHCFHAGRAVIDELEKNLQSHVAVASRMTLHFRGNT 470
OY 485 SSSGIWELAYMEAKESVYKDRVMOIARSGFKNSVYWKAMRKVKPTRRNNPWDCIN 544
Db 471 SSSSIWELAYIEAKGRKGRNVMOIARSGFKNSAVVALNNV-KPVSYSPEHCID 529
OY 545 RYVPL 550
Db 530 RYVPL 535

RESULT 5

US-09-883-797-12
; Sequence 12, Application US/09883797
; Patent No. US2002006123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 500
; TYPE: PR1
; ORGANISM: Arabidopsis thaliana
US-09-883-797-12

Query Match 50.8%; Score 1446.5; DB 10; Length 500;
Best Local Similarity 53.3%; Pred. No. 6.2e-126;
Matches 281; Conservative 94; Mismatches 111; Indels 41; Gaps 9;

OY 28 SPTSVRRRLPDFLOSVMKLYKLGHYHLYINHAVALYATPVLVLSAEVSLRSREI 87
Db 1 SPTVP---QAMPPESSSVKLYKLGHYHLYINHAVALYATPVLVLSAEVSLRSREI 56
OY 88 ---WKKLMDYLAIVY--GFGVFLTACVYFMSRPSRYLIIDFACYRPSDEHKTKEEF 142
Db 57 LNMWSTL-QPDLVOYGLSSFFVIFST--VYFMSRPTVLYADVSCYRPTVCTRPAT 113
OY 143 IELARKSGPDETLGFKRRILOASGIDETVYPRSSSENITMKGRREASVIFGA 202
Db 114 MEHSRLIKDKPKSVEFQMRILERSGLGETVYPAHLYIPTPTMDAARSAGVITREA 173
OY 203 LDELFEKTRVAKPDVGLVYVNCISFNPPLSAMVINHYKRGNTLSNLGSGSAGI 262
Db 174 MDLFEKTKGLPKPDVILVNCISLSPPLSAMVINHYKRGNTLSNLGSGSAGI 233
OY 263 AIDLARDMLQSNYSYAVVSTWGVGMVYVGSDDKSVIPNCFFFMGCSAVMLSNRRDF 322
Db 234 SVDLARDLQVHPNSNALTIVSTETIPYVGENEAMTLPLNCFMGAALHMSNRSD 293
OY 323 RHAKRYLEHIVTHKAADRSFVSVOEEDOGFKLISRDLMVEGEALKTNTITLGP 382
Db 294 WRAKYKLSLIVRTHGADKSPCYVEDEKRGHGINLSKDLMAIAGEALKANTITIGP 353
OY 383 LVLPSSEQLFPAALL-RRTSPAAKTSTTTSFSTATAKINGIKSSSDLSKRPIDYK 441
Db 354 LVLPSSEQLFPLTSLIGKIFNPK-----WKPIIPDK 386
OY 442 LAFFHCFHAAKSVYLELOKNLGLSEEMEASRMTLHFRGNTSSGIWELAYEAKES 501
Db 387 LAFFHCFHAGRAVIDELEKNLQSHVAVASRMTLHFRGNTSSSIWELAYEAKES 446
OY 502 VVRGDRVMOIARSGFKNSVYWKAMRKVKPTRRNNPWDCINRYV 548
Db 447 MRGRVMOIARSGFKNSAVVKNRTIKTP-KGPMPSDCIDRVPV 492

RESULT 6

US-09-892-325-4
; Sequence 4, Application US/09892325
; Patent No. US2002011673A1
; GENERAL INFORMATION:
; APPLICANT: Kunst et al.
; TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
; Involved in Very Long Chain Fatty Acid Synthesis
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

```

ADDRESS: Klargust Sparkman Campbell
          Leigh & Winston, LLP
STREET: One World Trade Center, Suite
          1600, 121 S.W. Salmon Street
CITY: Portland
STATE: OR
COUNTRY: USA
ZIP: 97204-2988

COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3.5-inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Word97 & ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/892,325
FILING DATE: 26-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/058,947
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: David J. Earp, Ph.D.
REGISTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 5493-50032/DUE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-892-325-4

Query Match          50.7%; Score 1445; DB 10; Length 497;
Best Local Similarity: 53.9%; Pred. No. 8,5e-126;
Matches 278; Conservative 93; Mismatches 107; Indels 38; Gaps 8;

QY 39 LPDFLOSVMKLYKGLYHNLINHAVALTIPVLVLSAEVGSLSREI--NKKLMDYD 95
DB 6 MPEFSSSVKLYKGLYHNLINHAVALTIPVLVLSAEVGSLSREI--NKKLMDYD 95
QY 96 LAIVI--GFGVVLVLAQYFEMSPRSVYIIDACIKPSEHKVYTKKEFIELARKSGFD 133
DB 64 LVQVLSSSEFVIFIST--VFEMSKPRITLYLVDSYCKPPTCYRVPFATFMEHSRLIKDK 121
QY 154 EETLGEKKRILOASGIGDETYVPRSSSENITTMKEGREGESVIFGALDELPEKTRVK 213
DB 122 PKVEQOMRIERSGIGEEICLPRAIHYIPPTTMDAANSEAOVIFEAAMDLPFKTGLK 181
QY 214 PKDGVLVVNCISIFNPTSLASAVINHYKRGNILSYNLGMCAGIILAIIDLARDMLOS 273
DB 182 PKDVLILVNCISIFNPTSLASAVINHYKRGNILSYNLGMCAGIILAIIDLARDMLOS 273
QY 274 NPSYAVVSTEVAVINHYGSDKSVIYPCFPRMCCSAVMSNRRRDFRHAYIRLEHIY 333
DB 242 HPSNMIIVSTELITPNYVQGNERAMLPCLERMGAALIHMSNRRSDRRAKYKLSHY 301
QY 334 RTHKADDSFRSVYOEDEOGFKGLISRDIMEVGEALKTITTLGLPVLVLPFSQDLF 393
DB 302 RTHRGADDSFYCYVYOEDEOGFHVGLINSLDMLAIGELAKNITITIGPLVLASQDLF 361
QY 394 PAAL--RTFSPPAKSTSTTSSTATAKTNGIKSSSSDLSKRYIPDYKLAFFHCFHAA 452
DB 362 LFTSLIRKILFNPK-----WKYIPDFKLAFFHCFIHAG 394
QY 453 SKVYLEELQKNLGLSENNKASMTLHRRGNTSSGIWELAYMEAKESVRRGRDRAWOIA 512
DB 395 GRAVIDEIQKNLQLSGEHVEASMTLHRRGNTSSSIWELAYIESKGRRRGRDRAWOIA 454
QY 513 FGSFGFNCNSVWKKAMKVKKPRNNPWVDCINRYPV 548

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DB 455 FGSFGFNCNSAVWKNRFTIKTP-KDGPMSDCIDRYPV 489

RESULT 7
US-09-883-797-2
Sequence 2, Application US/09883797
Patent No. US20020066123A1
GENERAL INFORMATION:
APPLICANT: Jaworski, Jan G.
APPLICANT: Post-Beltemiller, Martha A.
TITLE OF INVENTION: FATTY ACID ELONGASES
FILE REFERENCE: 07148/064001
CURRENT APPLICATION NUMBER: US/09/883,797
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 08/868,373
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 520
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-883-797-2

```

```

Query Match          50.5%; Score 1438; DB 10; Length 520;
Best Local Similarity: 51.4%; Pred. No. 4.1e-125;
Matches 265; Conservative 96; Mismatches 123; Indels 50; Gaps 10;

QY 6 EDDLSTETVNRGIEPSGPNAGSPFESVYRRLPDFLOSVMKLYKGLYHNLINHAVAL 63
DB 2 DRELTETEMAFR-----DSSAVIRIRRLPDLTSVKIKYVGLGHSNCVTTIL 52
QY 64 -YLATIP---VLYVLSAEVGSLSREIWK-KKLMDYDLATYVG--FEGVFLVLAQYFEM 115
DB 53 FFLIILPDTLVQLGLTFTFDS--ELMSNOAVOLDATRLCLVLSFVLT--LYVA 108
QY 116 SRPSVYLIDFACYKPSDEHKVYTKKEFIELARKSGKDEFTLFFKKRILOASGIGDETYV 175
DB 109 NRSKPYLVDFSCYKPKDEHKISVDSPLVMTENGSTDTDTVOQQRISRAGIGDETYL 168
QY 176 PRSISSENITTMKEGEESVYIFGALDELPEKTRVKPKDGVLVVNCISIFNPTSLA 225
DB 169 PRGITSPPRLNMSSEAAAEAVMFGALDSLFEKTGIKPAVEVILVNCISIFNPTSLA 228
QY 236 MVINHYKRGNILSYNLGMCAGIILAIIDLARDMLOSNSYAVVSTEVAVINHYGSDKSVI 295
DB 229 MIYNHYKMRDITSYNLGMCAGIILAIIDLARDMLOSNSYAVVSTEVAVINHYGSDKSVI 288
QY 296 DKSMVTPNCFPRMCCSAVMSNRRRDFRHAKYRLEHIVRTHKADDSFRSVYOEDEOG 355
DB 289 DRSMILCNCFRAGGAILLSNRDRBKSKSYLVVNVVRRHKSDDKNYCYQKDEERG 348
QY 356 FKGLKISRDIMEVGEALKTITTLGLPVLVLPSEQLFFAALIRTFSPPAKSTSTTSSES 415
DB 349 TIGVSLARELMSVAGALKNITITIGPMVPLPSEQLFISLIVK----- 393
QY 416 TSATATNGIKSSSSDLSKRYIPDYKLAFFHCFHAAKSVYLEELQKNLGLSENNKASR 475
DB 394 -----KMFKLK-----VKYIPDFKLAFFHCFIHAGGVAVLDEVOKNLDLKMHEPSR 442
QY 476 MTLHRRGNTSSGIWELAYMEAKESVRRGRDRAWOIAFGSGFNCNSVWKKAMKVK-KPT 534
DB 443 MTLHRRGNTSSSIWELAYMEATTEAKGKAGKADRDMQIAFGSGFNCNSAVKALRPVSTEEM 502
QY 535 RNNPWVDCINRYPV 548
DB 503 TGNAAWAGSIDQYVP 516

RESULT 8
US-09-877-476-42

```

RESULT 9
US-09-877-476-6
; Sequence 6, Application US/09877476
; Patent No. US2002004999A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.

```

RESULT 10
US-09-883-797-4
: Sequence 4, Application US/09883797
: Patent No. US20020086123A1
: GENERAL INFORMATION:
: APPLICANT: Jaworski, Jan G.
: APPLICANT: Post-Beltemmiller, Martha A.
: APPLICANT: Todd, James
: FILE OF INVENTION: FATTY ACID ELONGASES
: FILE REFERENCE: 07148/064001
: CURRENT APPLICATION NUMBER: US/09/883,797
: CURRENT FILING DATE: 2001-06-18
: PRIOR APPLICATION NUMBER: 08/868,373
: PRIOR FILING DATE: 1997-06-03
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 3.0.
: SEQ ID NO 4

```



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Db 1 MTSVN--VKLYRYVLTNFEINLCPLPLTAFL----AGKASRLTINDLHNLSTYLOHNL 53
QY 98 TVIGFEVFLACVYMSRPSRYLLIDFACYSKDEHKYTKKEFTIEL-----AR 147
Db 54 TVTLFFAFYVGLVLYTVTRPNPYLVDSYCLPPLHKVSVSKYMDIFYOIRKADTSSR 113
QY 148 KSGKFDDETLGFKRRILOASIGIDETVYVPRSSISSENTITMKEGREASTYIFGALDEL 207
Db 114 NVACDDPSSDLFLKRIODERGLDDETSPEGLIHVPRKFTFAASRETEKYITGALLEN 173
QY 208 EKTREKPDVGLVAVVNSIFNPPTSLSAMVINHYKMGNTILSYNLGMCAGIATDIA 267
Db 174 ENKRVNREIGILVYVNSMFPPTSLSAMVINHYKMGNTILSYNLGMCAGIATDIA 233
QY 268 RDMLOSPNSYAVVSTEMGYNMYVGSKSMVTPNCFPRGCSAVMLSNRRDPFRAXY 327
Db 234 KDLHVKRNTYALVSTENITNYIAGDNRSMVSNCLFRVGAAILLSNKPGRDRSKY 293
QY 328 RLEHIVTRKADRSFRSYQOEDEOGFKLISRLMEVGEALNTITTLPLVLPF 387
Db 294 ELVHTVTRHGADKSPRCVOQGDENGKIGVLSKIDTVAGRTVKNATLPLPL 353
QY 388 SEOLFFAALLRFTSPAAKTSTTSTSTATAKTNGIKSSSDLSKRYIPDYKLAEEH 447
Db 354 SEKLFFVTFM-----GKKLFKDKIKHYVDPFKLADHF 388
QY 448 CFHAASKVYLELOKNIGLSEENMEASRLTHRGNTSSSGIWEELAYMEAKESVRGDR 507
Db 389 CIHAGGAVIDLEKNTALAPIDVEASRSTLHREGNTSSSIWEELAYIEAKGMKKGK 448
QY 508 VMOIAFGSGFKCNSVWKAMRKVKKPTNNPWCINRPPPL 550
Db 449 VMOIALGSGFKCNSAVWVALNNVAKST-NSPWEHCIDRYPVKI 490

```

```

RESULT 13
US-09-877-476-40
; Sequence 40, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 506
; TYPE: PRY
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 173 amino acids from A. thaliana FA1 (SEQ ID
; OTHER INFORMATION: NO:2) and 3' 333 amino acids from B. napus
; OTHER INFORMATION: elongase KCS (SEQ ID NO:4) having a mutation at
; OTHER INFORMATION: residue 307; designated At1g3 G307D; hypothetical
US-09-877-476-40

```

```

Query Match 41.8%; Score 1190; DB 10; Length 506;
Best Local Similarity 45.5%; Pred. No. 4.5e-102;
Matches 238; Conservative 86; Mismatches 151; Indels 48; Gaps 6;
QY 43 LOSVNLKVKLGHYHLINHAUYLATIPVLVFSAEVGSLSREEL-----WKIMDYDIA 97
Db 1 MTSVN--VKLYRYVLTNFEINLCPLPLTAFL----AGKASRLTINDLHNLSTYLOHNL 53
QY 98 TVIGFEVFLACVYMSRPSRYLLIDFACYSKDEHKYTKKEFTIEL-----AR 147
Db 54 TVTLFFAFYVGLVLYTVTRPNPYLVDSYCLPPLHKVSVSKYMDIFYOIRKADTSSR 113

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QY 148 KSGKFDDETLGFKRRILOASIGIDETVYVPRSSISSENTITMKEGREASTYIFGALDEL 207
Db 114 NVACDDPSSDLFLKRIODERGLDDETSPEGLIHVPRKFTFAASRETEKYITGALLEN 173
QY 208 EKTREKPDVGLVAVVNSIFNPPTSLSAMVINHYKMGNTILSYNLGMCAGIATDIA 267
Db 174 KNTVNRKIDIGILVYVNSMFPPTSLSAMVINHYKMGNTILSYNLGMCAGIATDIA 233
QY 268 RDMLOSPNSYAVVSTEMGYNMYVGSKSMVTPNCFPRGCSAVMLSNRRDPFRAXY 327
Db 234 KDLHVKRNTYALVSTENITNYIAGDNRSMVSNCLFRVGAAILLSNKPGRDRSKY 293
QY 328 RLEHIVTRKADRSFRSYQOEDEOGFKLISRLMEVGEALNTITTLPLVLPF 387
Db 294 ELVHTVTRHGADKSPRCVOQGDENGKIGVLSKIDTVAGRTVKNATLPLPL 353
QY 388 SEOLFFAALLRFTSPAAKTSTTSTSTATAKTNGIKSSSDLSKRYIPDYKLAEEH 447
Db 354 SEKLFFVTFM-----GKKLFKDKIKHYVDPFKLADHF 388
QY 448 CFHAASKVYLELOKNIGLSEENMEASRLTHRGNTSSSGIWEELAYMEAKESVRGDR 507
Db 389 CIHAGGAVIDLEKNTALAPIDVEASRSTLHREGNTSSSIWEELAYIEAKGMKKGK 448
QY 508 VMOIAFGSGFKCNSVWKAMRKVKKPTNNPWCINRPPPL 550
Db 449 VMOIALGSGFKCNSAVWVALNNVAKST-NSPWEHCIDRYPVKI 490

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```

RESULT 14
US-09-877-476-34
; Sequence 34, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 506
; TYPE: PRY
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 506 amino acids from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO:4) having a mutation at residue 307; designated
US-09-877-476-34

```

```

Query Match 41.7%; Score 1187; DB 10; Length 506;
Best Local Similarity 44.8%; Pred. No. 8.6e-102;
Matches 233; Conservative 98; Mismatches 147; Indels 42; Gaps 7;
QY 43 LOSVNLKVKLGHYHLINHAUYLATIPVLVFSAEVGSLSREELWKIMDYDIA 99
Db 1 MTSVN--VKLYRYVLTNFEINLCPLPLTAFL----AGKASRLTINDLHNLSTYLOHNL 56
QY 100 IGFGVFLVACVYMSRPSRYLLIDFACYSKDEHKYTKKEFTIEL-----ARKSG 151
Db 57 APLFAFYVGLVLYATPRKPYLVLYEYSCYLPFRHCRSSISKVMDIFYOVRKADPSRNGT 116
QY 152 FDEEL-LGFKRRILOASIGIDETVYVPRSSISSENTITMKEGREASTYIFGALDEL 210
Db 117 CDDSSWMLDLKRIODERGLDDETSPEGLIHVPRKFTFAASRETEKYITGALLEN 176
QY 211 RVPKPDVGLVAVVNSIFNPPTSLSAMVINHYKMGNTILSYNLGMCAGIATDIA 270

```

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Db 177 NVNRKDIGILVNSMFMPTSLAMVNVTFKLSNVFSNLGCGCAGVIALDLADL 236
QY 271 LOSPNISAAVYVSTEMGYNMYVSDKSMVLPNCFEFRGCAVMSNRNDRFRRAKYLE 330
Db 237 LHVKNKYALVYVSTEMTNTYNTIYACDNRSMVSNCLFRVGGAAIILSNPGRDRSRKYLEV 296
QY 331 HAVTHAAADDRFSRYVQEEDEOGFKLISRDIMEVGEALKTNTTGLPLPSPSQ 390
Db 297 HAVTHGADDSFRVQGGDENGKIGVLSKIDITVAGHTYAKNTATLGLPLPSEK 356
QY 391 LLEFPAALLRTFSPAATSTTTSTFSATKTNKIGKSSSDLSKPYIPDYKLAPEHCFH 450
Db 357 LLEFVTFM-----GKLFKDKIKHYVYDPFKLADHCH 391
QY 451 AASKVYLELOKNLGLSEENMEASBMTLHREGNTSSGITYELAYEAKESVRRGRDVMQ 510
Db 392 AGGRAVIDLEKMLALAPIDVEASRSTLHREGNTSSSIYELAYEAKGMRKKNVMO 451
QY 511 IAFSGFKCNSVVKAMRKVKKPTRRNPNWDCINRYVPVL 550
Db 452 IAFSGFKCNSAVWVALNWKAST-NSPWEHCIDRIYVKI 490

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RESULT 15

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US-09-877-476-2
; Sequence 2, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-877-476-2

```

Query Match 41.6%; Score 1186; DB 10; Length 506;
Best Local Similarity 45.5%; Pred. No. 1.1e-101;

Matches 238; Conservative 87; Mismatches 150; Indels 48; Gaps 6;

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QY 43 LOSVNLKYVGLGYHLLINHAVALTIPVLVLSAEVGSLSREI-----WKKLMDYDLA 97
Db 1 MTSVN--VLLRYVYLTNFENCLPPLTFL---AGKASRLTINDLHNFSLYLQHNLI 53
QY 98 TVIGFGVFLVACVYFMSRPSVYLIDFACYPSDEHKVYKKEFTL-----AR 147
Db 54 TVTLTALFTVGLVLYTRPNVYLVDSYCLPPHLKVSYSKVDIDFYQIKKADTSR 113
QY 148 KSGKFEDELGFKKRILOASIGDETYVPRSSISENITMKGREASTVIFGALDEL 207
Db 114 NVACDPPSLDLFRKIOERSGLADETSPBGLIHVPRKTFPAASRETEKVIIGALENLF 173
QY 208 EKTRVAKVGVLYVNCISIFNPPLSLAMVINHYKRGNTLSYNLGMCAGIITADLA 267
Db 174 EMTKYVPREIGILVNSMFPPLSLAMVNTFKLSNKSFNGLGMCAGIITADLA 233
QY 268 RDLQSNPNSVAVVSTEMVGNMYVSDKSMVLPNCFEFRGCAVMSNRNDRFRRAKYLE 327
Db 234 KDLHVHKNKYALVYVSTEMITOGIYAGEBRSMMVSNCLFRVGGAAIILSNKSGDRRSKY 293
QY 328 RLEHIVRTHKADDSFRSVQEEDEOGFKLISRDIMEVGEALKTNTTGLPLPSPSQ 387
Db 294 KLVHIVRTHGADDSFRVQGGDENGKIGVLSKIDITVAGHTYAKNTATLGLPLPSEK 353

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```

QY 388 SEQLLEFPAALLRTFSPAATSTTTSTFSATKTNKIGKSSSDLSKPYIPDYKLAPEH 447
Db 354 SEKLEFPAATSTTTSTFSATKTNKIGKSSSDLSKPYIPDYKLAPEH 388
QY 448 CFHASKVYLELOKNLGLSEENMEASBMTLHREGNTSSGITYELAYEAKESVRRGRD 507
Db 389 CIHAGRAVIDLEKMLALAPIDVEASRSTLHREGNTSSSIYELAYEAKGMRKKNVMO 451
QY 508 VMOIAFSGFKCNSVVKAMRKVKKPTRRNPNWDCINRYVPVL 550
Db 449 AMOIALGSGFKCNSAVWVALNWKAST-KASANSPPWCHIDRIYVKI 490

```

Search completed: May 11, 2003, 01:33:12
Job time: 614 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2003, 22:59:09 ; Search time 589 Seconds

(Without alignments)
89.769 Million cell updates/sec

Title: US-09-905-657-2

Perfect score: 2848

Sequence: 1 MGRSNEODLLSTEIVNRGIE.....KKPTRRNPWVCINRYPVPL 550

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73.*
2: PIR1.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2848	100.0	550	2	B84658	beta-ketoacyl-CoA
2	1569	55.1	516	2	F86327	protein F18014.21
3	1494.5	52.5	509	2	A84653	probable beta-keto
4	1492	52.4	512	2	F84538	probable beta-keto
5	1459	51.2	528	2	T00951	probable 3-oxoacyl
6	1445	50.7	497	2	T52308	very-long-chain fa
7	1441	50.6	528	2	F86141	protein T25K16.11
8	1402	49.2	487	2	T05271	probable 3-oxoacyl
9	1372	48.2	492	2	F86384	probable protein f
10	1213	42.6	451	2	T49095	beta-ketoacyl-CoA
11	1197.5	42.0	505	2	T07900	probable 3-oxoacyl
12	1196.5	42.0	466	2	D84906	probable beta-keto
13	1194	41.9	493	2	T04771	fatty acid elongas
14	1186	41.6	506	2	T05272	fatty acid elongas
15	1180	41.4	506	2	T07934	probable 3-oxoacyl
16	1170.5	41.1	476	2	H84524	probable fatty aci
17	1005.5	35.3	460	2	C96736	probable ketoacyl-
18	844	29.6	478	2	D86212	hypothetical prote
19	822	28.9	464	2	T48449	fatty acid elongas
20	817.5	28.7	476	2	C84687	probable fatty aci
21	495.5	17.4	168	2	T07846	probable beta-keto
22	486.5	17.1	168	2	T07845	beta-ketoacyl synt
23	482.5	16.9	168	2	T14434	probable beta-keto
24	481.5	16.9	168	2	T14385	fatty acid elongas
25	213	7.5	438	2	A69593	naringenin-chalcon
26	181.5	6.4	365	2	B97339	naringenin-chalcon
27	179	6.3	325	2	G70621	3-oxoacyl-lacyl-ca
28	175	6.1	353	2	G70621	probable chalcons
29	167	5.9	388	2	S60472	naringenin-chalcon

30	166.5	5.8	388	1	SYSCN	naringenin-chalcon
31	166.5	5.8	388	2	JQ2259	naringenin-chalcon
32	166	5.8	391	2	T10713	naringenin-chalcon
33	163.5	5.7	388	1	SYSC1	naringenin-chalcon
34	163	5.7	388	2	JQ2249	naringenin-chalcon
35	160.5	5.6	324	2	D81452	3-oxoacyl-lacyl-ca
36	156	5.5	388	1	SYSC3	naringenin-chalcon
37	156	5.5	390	2	T10231	another-specific pr
38	156	5.5	398	2	S42523	naringenin-chalcon
39	156	5.5	402	2	S5465	chalcone synthase
40	154.5	5.4	389	1	SYFUCP	naringenin-chalcon
41	154	5.4	363	2	T15054	another-specific pr
42	154	5.4	419	1	SYPCD	naringenin-chalcon
43	153	5.4	388	2	S37098	naringenin-chalcon
44	153	5.4	389	2	S35163	naringenin-chalcon
45	153	5.4	392	2	S53313	stilbene synthase

ALIGNMENTS

RESULT 1
B84658
beta-ketoacyl-CoA synthase (FIDLEHEAD) [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: B84658

Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.
M.; Koo, H.; Mofat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayan, L.; Tallon
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vent
Nature 402, 761-768, 1999

Attiter-Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: B84658

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-550 <STO>

A:Cross-references: GB:A8002093; NID:g3075394; PIDN:AC14526.1; GSPDB:GN0139

C:Genetics:

A:Gene: At2g26250

A:Map position: 2

Query Match	Best Local Similarity	100.0%	Score 2848	DB 2	Length 550
Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY	1	MGRSNEODLLSTEIVNRGIEPSGNAGSPFESVRRRLPDFLQSVNLRKYKLGHYLIN 60			
DB	1	MGRSNEODLLSTEIVNRGIEPSGNAGSPFESVRRRLPDFLQSVNLRKYKLGHYLIN 60			
OY	61	HAVYATTPVLVLSAEVGSLSREIWKIMDYDLATVIGFGVFLACVYFMSRPS 120			
DB	61	HAVYATTPVLVLSAEVGSLSREIWKIMDYDLATVIGFGVFLACVYFMSRPS 120			
OY	121	VYLIDFACYPKDEHKVTKKEEFLIARKSGKDEETLGKRIILQASGIDETVYPRIS 180			
DB	121	VYLIDFACYPKDEHKVTKKEEFLIARKSGKDEETLGKRIILQASGIDETVYPRIS 180			
OY	181	SENTITMKEGREASTVIFGALDELFEKTRVAPKDVGVLVVNCISFNPPTSLAMVINH 240			
DB	181	SENTITMKEGREASTVIFGALDELFEKTRVAPKDVGVLVVNCISFNPPTSLAMVINH 240			
OY	241	YKMRNITLSYNGMGCSAGIIDLARDMLQSNSTAVVSTVMGVMNVGSDKSMV 300			
DB	241	YKMRNITLSYNGMGCSAGIIDLARDMLQSNSTAVVSTVMGVMNVGSDKSMV 300			
OY	301	IPNCFRFGCSAVMLSNRRDFRHAQYRLHIVRTHKAADRSFVSYYOEDEQGFGLK 360			
DB	301	IPNCFRFGCSAVMLSNRRDFRHAQYRLHIVRTHKAADRSFVSYYOEDEQGFGLK 360			
OY	361	ISRDLMEVGGAALKTNITTLGLVLPFSQQLFPFALLRRFSPPAKSTTTSSTSAFA 420			
DB	361	ISRDLMEVGGAALKTNITTLGLVLPFSQQLFPFALLRRFSPPAKSTTTSSTSAFA 420			

QY 421 KINGISSSSDLSKPIPYKLAFFHCFHFAASKVYLELOKNIQISEENMEASRMTLHR 480
 DB 421 KINGISSSSDLSKPIPYKLAFFHCFHFAASKVYLELOKNIQISEENMEASRMTLHR 480
 QY 481 FGNSSSGIWEYELAYWEAKESVRRGRVQIAFGSGFKNSVYKAMRKVKRPTNNPV 540
 DB 481 FGNSSSGIWEYELAYWEAKESVRRGRVQIAFGSGFKNSVYKAMRKVKRPTNNPV 540
 QY 541 DCINRYPVPL 550
 DB 541 DCINRYPVPL 550

RESULT 2

Protein F18014.21 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 R:Phenology: A.; Ecker, J.R.; Palm, C.J.; Federle, N.A.; Kaul, S.; White, O.; Alonso,
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maltl, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: F86327
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-516 <STO>
 A:Cross-references: GB:AE005172; NID:98778420; PIDN:AAF9428.1; GSPDB:GN00141
 A:Genetics:
 A:Gene: F18014.21
 A:Map position: 1

Query Match

Best Local Similarity 55.1%; Score 1569; DB 2; Length 516;
 Matches 300; Conservative 82; Mismatches 117; Indels 32; Gaps 5;

QY 23 GPNAGSTFVSRRRLPDLQSVNLKYGHYLNHAYLATIPVLVFSAEVGS 82
 DB 13 GGGDSVGVQIRQRMPLDFQSVNLKYGHYLNHAYLATIPVLVFSAEVGS 71
 QY 83 SREIRWKLW---DYDLATVIGFGVFLVACVYFMSRPSVYLIDPACIKPSDEHKVTK 139
 DB 72 NPDDL KQIMHLOYNLVSITILCSAILVFGILVYVMTRRPVYLVDFSCYLPDHLKAPY 130
 QY 140 EEFTELARKSGKDETLGFKRRILOASGIDETVYPRSSISENITTMKREGREASTVI 199
 DB 131 ARMEHRLTGFDDSLAEQKRLKILSGEDIVYEAHMYPPRIISMAAREADV 190
 QY 200 FGLDELFEFTRKPKDGVVYVNCSTFNPPLSAMVINHYKMGNTLSYNLGMCSSA 259
 DB 191 FGLDMLFANTVYKPKDIGILVNCSTFNPPLSAMVINHYKMGNTLSYNLGMCSSA 250
 QY 260 GIAIDARDMLQSNVYAVVSTEWGYNVVGSKSVYITNCFRMCSSAVMLSNRR 319
 DB 251 GYAVLADMLVHRTATVAVVSTENITQNWYFGNKKSMILPNCLEFRVGSVLLSNKS 310
 QY 320 RDRFAKYLRLHIVTRHKAADRSFRSVYOEDEOGFKGISRDIMEVGEALKTNTT 379
 DB 311 RDRKRSKYLRLHIVTRHKAADRSFRSVYOEDEOGFKGISRDIMEVGEALKTNTT 370
 QY 380 LGPLVLPSEDLLEFALLRRTFSPAKSTSTTSFSTATAKNGIKSSSDLSKPIYD 439
 DB 371 LGPLVLPSEDLLEFALLRRTFSPAKSTSTTSFSTATAKNGIKSSSDLSKPIYD 404
 QY 440 YKLAFHCFHFAASKVYLELOKNIQISEENMEASRMTLHFRGNTSSSGIWEYELAYWEAK 499

DB 405 FKLAFFHCFHAGRAVIELEKNQLSPVYAEASRMTLHFRGNTSSSGIWEYELAYWEAK 464
 QY 500 ESVRGRDVRVQIAFGSGFKNSVYKAMRKVKRPTNNPVDCINRYPVPL 550
 DB 465 GRMRGRDVRVQIAFGSGFKNSVYKAMRKVKRPTNNPVDCINRYPVPL 514

RESULT 3

Protein beta-ketoacyl-CoA synthase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 R:Phenology: A.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Unayam, L.; Tallon,
 eus, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: A84663
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-509 <STO>
 A:Cross-references: GB:AE002093; NID:92760830; PIDN:AA95298.1; GSPDB:GN00139
 A:Genetics:
 A:Gene: AC2426640
 A:Map position: 2

Query Match

Best Local Similarity 52.5%; Score 1494.5; DB 2; Length 509;
 Matches 283; Conservative 86; Mismatches 112; Indels 33; Gaps 5;

QY 37 RRLDFQSVNLKYGHYLNHAYLATIPVLVFSAEVGSLSREIRWKLW--- 93
 DB 15 RRLDFQSVNLKYGHYLNHAYLATIPVLVFSAEVGSLSREIRWKLW--- 72
 QY 94 YDLATVIGFGVFLVACVYFMSRPSVYLIDPACIKPSDEHKVTK 153
 DB 73 YNLISVAVCSMLVFLMTIYFMTRRPVYLVNFCFPRDESCKTKIFMDRSKLTGSET 132
 QY 154 EETLGFKRRILOASGIDETVYPRSSISENITTMKREGREASTVI 213
 DB 133 EENLEFQKRILOASGIDETVYPRSSISENITTMKREGREASTVI 192
 QY 214 PKDGVVYVNCSTFNPPLSAMVINHYKMGNTLSYNLGMCSSAGIATDLARDMLQS 273
 DB 193 PKDIGILVNCSTFNPPLSAMVINHYKMGNTLSYNLGMCSSAGIATDLARDMLQS 252
 QY 274 NPNSYAVVSTEWGYNVVGSKSVYITNCFRMCSSAVMLSNRRDPRHAKYRLHIV 333
 DB 253 IPNTYAVVSTEWGYNVVGSKSVYITNCFRMCSSAVMLSNRRDPRHAKYRLHIV 312
 QY 334 RTHKAADRSFRSVYOEDEOGFKGISRDIMEVGEALKTNTT 393
 DB 313 RTHKAADRSFRSVYOEDEOGFKGISRDIMEVGEALKTNTT 372
 QY 394 FALLL-RTFSFAKSTSTTSFSTATAKNGIKSSSDLSKPIYDYLKLAFFHCFHFA 452
 DB 373 FALVGRKLEFKMKI-----KYLIDFKLAFFHCFHFA 405
 QY 453 SKYVLELOKNIQISEENMEASRMTLHFRGNTSSSGIWEYELAYWEAKESVRRGRVQIA 512
 DB 406 GRVAVLELOKNIQISEENMEASRMTLHFRGNTSSSGIWEYELAYWEAKESVRRGRVQIA 465
 QY 513 FGSFGKNSVYKAMRKVKRPTNNPVDCINRYPV 548
 DB 466 FGSFGKNSVYKAMRKVKRPTNNPVDCINRYPV 501

RESULT 4

F84538
 probable beta-ketoacyl-CoA synthase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: F84538
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Nierman, M.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: F84538
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-512 <STO>
 A:Cross-references: GB:AE002093; NID:g4544399; PIDN:AAD22309.1; GSPDB:GN00139
 A:Genetics:
 A:Gene: Atg216280
 A:Map position: 2

Query Match 52.4%; Score 1492; DB 2; Length 512;
 Best Local Similarity 54.1%; Pred. No. 6.2e-104;
 Matches 280; Conservative 100; Mismatches 106; Indels 32; Gaps 6;

```

QY 36 RRRLPDLQSVNLKYYKLGHYHLINHAAYLATIPVLVFSAEVGSLSREELMKLM--- 92
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 22 RRRLPDLQSVNLKYYKLGHYHLINHAAYLATIPVLVFSAEVGSLSREELMKLM--- 92
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 93 DYLAIVGFYFVLTACVYFMSRPSRYLLIDPACYPDEHKVTEKEETELARKSGKF 152
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 QYDLVAFIFLSALAFESGYIYIMSRPSRYLLIDPACYPDEHKVTEKEETELARKSGKF 139
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 153 DEETLFGKRIILQASGIDETVYPRSSISENTITMKREGEASTVIFGALDELFEKTRV 212
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 NESLEFQRILERSGIDETVYPRSSISENTITMKREGEASTVIFGALDELFEKTRV 199
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 213 KRPDVGVLVNCISFNTPSLAMVINHYKMGNTISYNGMGCSAGIATIDARMDLQ 272
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 200 NRPDVGVLVNCISFNTPSLAMVINHYKMGNTISYNGMGCSAGIATIDARMDLQ 259
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 273 SNRPSYAVVSTEWGYNVYVSGDSKSVIPNCFPRMGCSAVMLSNRRDRFNAKYLEHIV 332
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 260 VHRNTAVVSTENITONMTFGKNAKMLIPNCFPRMGCSAVMLSNRRDRFNAKYLEHIV 319
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 333 VTRHKAADRSFRSYVQEEDEQGFGLKISRDLMVEGGLKNTITLGPVLPFSBQL 392
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 320 VTRHKAADRSFRSYVQEEDEQGFGLKISRDLMVEGGLKNTITLGPVLPFSBQL 379
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 393 FFALLRRTSPAKTSTTTSFSTAKTNGIKSSSDLSKPIIPYKIAFEHCFHAA 452
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 380 FFALLRRTSPAKTSTTTSFSTAKTNGIKSSSDLSKPIIPYKIAFEHCFHAA 413
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 453 SKVLEELQKNGISEENMEASRMTLHRFGNTSSGIWELAYVEAKESVRGDRWQIA 512
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 414 GRAVIDLEKNIQSLQHVASRMTLHRFGNTSSGIWELAYVEAKESVRGDRWQIA 473
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 513 FGSFGKCNVYKAMRKRYKPTNNPWCINRYVPVL 550
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 474 FGSFGKCNVYKAMRKRYKPTNNPWCINRYVPVL 510
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 5

T00951
 Probable 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) F20D22.1 - Arabidopsis
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Jul-1999
 C:Accession: T00951
 R:Vysotskaya, V.S.; Osborne, B.I.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji,
 K.; Peng, J.; Kim, C.; Kurtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.;
 submitted to the EMBL Data Library, May 1998
 A:Description: Arabidopsis thaliana chromosome 1 BAC F20D22 complete sequence.
 A:Reference number: Z14214
 A:Accession: T00951
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-528 <VYS>
 A:Cross-references: EMBL:AC002411; NID:g2570223; PID:g3142289
 C:Accession: F84538
 A:Map position: 1
 A:Introns: 256/3
 A:Note: F20D22.1
 C:Keywords: acyltransferase

Query Match 51.2%; Score 1459; DB 2; Length 528;
 Best Local Similarity 53.4%; Pred. No. 1.9e-101;
 Matches 278; Conservative 91; Mismatches 120; Indels 32; Gaps 5;

```

QY 37 RRRLPDLQSVNLKYYKLGHYHLINHAAYLATIPVLVFSAEVGSLSREELMKLM--- 92
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 RRRLPDLQSVNLKYYKLGHYHLINHAAYLATIPVLVFSAEVGSLSREELMKLM--- 92
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 96 LATVIGFVYFVLTACVYFMSRPSRYLLIDPACYPDEHKVTEKEETELARKSGKF 155
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 LATVIGFVYFVLTACVYFMSRPSRYLLIDPACYPDEHKVTEKEETELARKSGKF 139
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 156 TIGPKRIILQASGIDETVYPRSSISENTITMKREGEASTVIFGALDELFEKTRV 215
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 TIGPKRIILQASGIDETVYPRSSISENTITMKREGEASTVIFGALDELFEKTRV 199
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 216 DVGVLVNCISFNTPSLAMVINHYKMGNTISYNGMGCSAGIATIDARMDLQSNP 275
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 200 DVGVLVNCISFNTPSLAMVINHYKMGNTISYNGMGCSAGIATIDARMDLQSNP 259
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 276 NSYAVVSTEWGYNVYVSGDSKSVIPNCFPRMGCSAVMLSNRRDRFNAKYLEHIV 335
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 260 NSYAVVSTEWGYNVYVSGDSKSVIPNCFPRMGCSAVMLSNRRDRFNAKYLEHIV 319
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 336 HKAADRSFRSYVQEEDEQGF--GLKISRDLMVEGGLKNTITLGPVLPFSBQL 393
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 320 HKAADRSFRSYVQEEDEQGF--GLKISRDLMVEGGLKNTITLGPVLPFSBQL 379
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 394 FFALLRRTSPAKTSTTTSFSTAKTNGIKSSSDLSKPIIPYKIAFEHCFHAA 453
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 380 FFALLRRTSPAKTSTTTSFSTAKTNGIKSSSDLSKPIIPYKIAFEHCFHAA 414
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 454 KVLLEELQKNGISEENMEASRMTLHRFGNTSSGIWELAYVEAKESVRGDRWQIA 513
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 415 KVLLEELQKNGISEENMEASRMTLHRFGNTSSGIWELAYVEAKESVRGDRWQIA 474
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 514 GSGFGKCNVYKAMRKRYKPTNNPWCINRYVPVL 550
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 475 GSGFGKCNVYKAMRKRYKPTNNPWCINRYVPVL 515
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 6

T52308
 very-long-chain fatty acid condensing enzyme CUT1 [validated] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
 C:Accession: T52308
 R:Miller, A.A.; Clemens, S.; Zachgo, S.; Giddins, M.; Taylor, D.C.; Kunst, L.
 Plant Cell 11, 825-838, 1999
 A:Title: CUT1, an Arabidopsis gene required for cuticular wax biosynthesis and pollen
 A:Reference number: Z26032; MUID:99264304; PMID:10330468
 A:Accession: T52308
 A:Status: preliminary;
 A:Molecule type: mRNA
 A:Residues: 1-497 <MTL>
 A:Cross-references: EMBL:AF129511; PIDN:AAD7122.1
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Gene: CUT1
 C:Function:
 A:Description: necessary for cuticular wax production [validated, MUID:99264304]; prc

Query Match 50.7%; Score 1445; DB 2; Length 497;
 Best Local Similarity 53.9%; Pred. No. 2e-100;
 Matches 278; Conservative 93; Mismatches 107; Indels 38; Gaps 8;

[illegible]

RESULT 8
T05271

RESULT 8
 T05271
 probable 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) - *Arabidopsis thaliana*
 N/Alternate names: ketoacyl-CoA synthase; protein T4L20.90
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
 C/Accession: T05271
 R/evan, M.; Terryn, N.; Ardiles, W.; Buyschaert, C.; Dasseville, R.; De Clerck, R.,
 ewes, H.W.; Mayer, K.F.X.; Schueller, C.
 submitted to the Protein Sequence Database, September 1998
 A/Reference number: Z15406
 A/Accession: T05271
 A/Molecule type: DNA
 A/Residues: 1487 <BEV>
 A/Cross-references: EMBL:AL023094
 A/Experimental source: cultivar Columbia; BAC clone T4L20
 C/genetics:
 A/Map position: 4
 A/Note: T4L20.90
 C/Keywords: acyltransferase

Query Match 49.2%; Score 1402; DB 2; Length 487;
 Best Local Similarity 53.7%; Pred. No. 3.2e-97;
 Matches 273; Conservative 89; Mismatches 102; Indels 44; Gaps 8;

Db 15 YKLTGTHLTHFEKTLMLPLMAVLFMNVLSTLSLNLHLY-----YNGT---GF--IIVI 64
 QY 109 T-----ACVYENSRPSRYLLIDFACYKSPDEKHXKEEFIELARSGKFEDETLGFKRI 16
 Db 65 TLAIVGSIVTFEKSRSRSTYLLDSCYLPSSQKVSQKFMNNSLIDQSTLSLEFKRI 12
 QY 164 LQASIGDETVVPRISSENITMKBEREASAYIVIGALDELFEKTRVPRKDGVLVN 22
 Db 125 LIRSLGSETYLPDSIHSLIPRPILMAAREAEVIGALDNLINREKRIINREIGVLVN 18

Db 351 -----EPGFHICVLASSKKVLDIHKDKLLEENMEASRTLERFGNTSSSI 399

QY 490 WYELAYEAKSVRGDRWQIAFGSGKCNVYWKAMRKVKPTRRNPW 539

Db 400 WYELAYLEHAKMKGRWQIGFGSGKCNVYWKALKKIDPPRRNPW 449

RESULT 11

T07900

Probable 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) FAE1 - rape

N/Alternate names: 3-ketoacyl-CoA synthetase; fatty acid elongase

C/Species: Brassica napus (rape)

C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999

C/Accession: T07900

R/Roscoe, T.J.; Domergue, F.; Lessire, R.; Delseeny, M.

submitted to the EMBL Data Library, March 1996

A/Reference number: Z16199

A/Accession: T07900

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1505 <ROS>

A/Cross-references: EMBL:U05071; NID:G1255206; PIDN:AAA96054.1; PID:G1255207

C/Genetics:

A/Genes: FAE1

C/Function:

A/Description: catalyzes the transfer of malonyl from malonyl-CoA to the fatty acid chain

A/Pathway: fatty acid synthesis

C/Keywords: acyltransferase

Query Match

Best Local Similarity 42.0%; Score 1197.5; DB 2; Length 505;

Matches 225; Conservative 96; Mismatches 146; Indels 43; Gaps 7;

QY 43 LOSYNLKYKLGHYLLINHAVALTIPVLVFSAEVGSLSREIWKLMYD---DLATV 99

Db 1 MTSIN--VKLLHYVTNLFNLCFFPLTAIV--AGKAYLTIDDLHLHYSLQHNLIIT 55

QY 100 IGFEGVFLVACVYFENRPSVYLIDPACYKPSDEHKVTKKEEFL-----ARKSGK 151

Db 56 APLLAFVFSGLVIAIRPRPVYLVESCVLPTRHSSISIKVNDIFFOYKADPSRNGT 115

QY 152 FDEET-LGFKRRILOAGSIDETVYVPRSSISENITMKREGEASVIFGALDELPEKT 210

Db 116 CDDSMWDLFRKIQERSGLDETHGPGGLQVPRKTFARARETEQVYIIGALENLKNT 175

QY 211 RYVPRKDVGLVNCSTINPTPSLAVYINHYKMGKNTLSNLSGSGSAGIATDARDM 270

Db 176 NVNPKVDIGILVNVSSMENPPSLSAMVYNTFKLSNVSRFNLGSGSAGIATDARDM 235

QY 271 LOSNPNSYAVVSTFEMVGYMMVYGSQSVIIPNCFRFGCSAVWLSNRDRDFRAKTRLE 330

Db 236 LHVHKNYALVSTENITVITAGDNRSMAVSNCLFVVGGAAILSKPRDRRSKTELV 295

QY 331 HAVRTHAADRSFVYQDEDEGFGKLGKISRDLMVEGGEALNTNTTIGPLVLPSEQ 390

Db 296 HTVHTHGADKSPRCVQGDDEGCGVSLNDITVDARIVYKKNATIGPLILPSEK 355

QY 391 LLEFPAALLRRTFSPAAKTSTTTSATKATKICSSSDLSKPYIPDYKLAHEHCFH 450

Db 356 LLEFVTFM-----GKLFKDEIKHYVPPDEKLADHFCIH 390

QY 451 AASKVYLEELQKNIIGSEENMEASRMTLHREGNTSSGIVYELAYMAKESVRGDRWQ 510

Db 391 AGKAAVIVLEKNIIGLAPIDVEASRSLHFRGNTSSSIYELAYIPKRMKGNKRWQ 450

QY 511 IAFSGFKCNVYWKAMRKVKPTRRNPWDCINRPVPL 550

Db 451 IALGSGFKCNVYWKAMRKVKPTRRNPWDCINRPVPL 550

RESULT 12

DB4906

Probable beta-ketoacyl-CoA synthase [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C/Accession: D84906

R/lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Koo, H.; Moffat, K.S.; Crobin, L.A.; Shen, P.; Vanaken, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: D84906

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1466 <STO>

A/Cross-references: GB:AE002093; NID:G3831446; PIDN:AA69929.1; GSPDB:GN00139

A/Genes: At2g46720

A/Map position: 2

Query Match 42.0%; Score 1196.5; DB 2; Length 466;

Best Local Similarity 45.8%; Pred. No. 7.7e-82;

Matches 228; Conservative 105; Mismatches 116; Indels 49; Gaps 7;

QY 63 VYLAIPVLYVFSAEVGSLSREIWKLMYDILATV-IGFEGV-----VLTACVYF-- 114

Db 3 IAMDFFKILIL-----LILSFLDLHLHHDFSPFVKIGLILSIFVYA 51

QY 115 --MSRPSRVYIDPACYKPSDEHKVTKKEEFLARKSGKPEDETLGFKRRILOAGSID 172

Db 52 YSTRSKPVYLVDSHQPTDSCKISSEFFENMAKQALYDEITIQMTRLNNSGIGDD 111

QY 173 TYVRSISISSNITMKREGEASVIFGALDELPEKTRVAKVGLVNCSTINPTPS 232

Db 112 TYSRCKMLTSPPTSMYEAHRESELVIFGALNSLFKRTGIEPRRGVIFIVNCSLFNPNPS 171

QY 233 LSAMVINYKMGKNTLSNLSGSGSAGIATDARDMLOSNPNSYAVVSTFEMVGYMMVY 292

Db 172 LSSMIVNRYKIDVYKTNLSGSGSAGIATDARDMLOSNPNSYAVVSTFEMVGYMMVY 231

QY 293 VGSQSVIIPNCFRFGCSAVWLSNRDRDFRAKTRLEHIVTRKADDSFRSYOED 352

Db 232 RGNDRSMVLPNCLEFRVGAAMVLSNRSDQVRSYELTHIVTRKSGSDKHYTCAEKED 291

QY 353 EOGKGLKISRDLMVEGGEALNTNTTIGPLVLPSEQLFPALLRRTSSPAKTSITT 412

Db 292 SKGIVGALSLELTVAGDSIKTMTALGPLVLPSEKLEFIFLVK----- 338

QY 413 SFTSATATNGIKSSSDLSKPYIPDYKLAHEHCFHAASKVYLEELQKNIIGSEENME 472

Db 339 -----SKLFRKLV-----PVPDFKLCFKHFCIHAGGRALLDAVERGLISEFDLE 385

QY 473 ASRMTLHFRGNTSSGIVYELAYMAKESVRGDRWQIAFGSGFKCNVYWKAMRKV-- 530

Db 386 PSRMTLHFRGNTSSSILWEYELAYEAKCRVGRDRWQIAFGSGFKCNSTYMRALRTIPA 445

QY 531 KKPTRNNPWCINRPV 548

Db 446 NESLVNPMGDSVHKYV 463

RESULT 13

T04771

fatty acid elongase homolog F10M10.20 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999

C/Accession: T04771

R/Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Hohelsel, J.; Meves, H.W.; May

submitted to the Protein Sequence Database, February 1999

A/Reference number: Z15384

A/Accession: T04771

A/Molecule type: DNA

A/Residues: 1493 <BEV>

A/Cross-references: EMBL:AL035521

A/Experimental source: cultivar Columbia; BAC clone F10M10

Query Match	41.6%	Score 1186;	DB 2	Length 506;
Best Local Similarity	45.5%;	Pred. No. 5.3e-81;		
Matches 238; Conservative	87;	Mismatches 150;	Indels 48;	Gaps 6

OY	43	LSVN	LKTVK	LG	HYH	LN	HA	VY	LT	PV	LV	LV	SA	EV	GS	LS	RE	E	---	W	R	K	L	M	D	Y	D	L	A	97											
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:												
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db	1	MTSV	---	V	K	L	R	V	L	I	N	F	N	C	I	C	F	P	L	A	F	---	A	G	A	S	A	T	I	D	N	L	F	S	Y	L	O	H	N	I	53

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Db 237 LHVKNNTYALVSTENITYAGDNRSMVSNCLFRVGAAILSNKPGDRRSKYEIV 296
QY 331 HIRTHKAAADDRSFPSVYOEDEOGFKGLKTSRDLMEVGEALKTNTITLGPVLPFSEQ 390
Db 297 HTVTHHGADGKSFRCVQOGDENGKIGVSLSKDITDVGRTYKKNITLIGPLILPSEK 356
QY 391 LFFPAALLRRTFSPAKTSTTSTSATAKTNGIKSSSDLSKPYIPDYKLAFFHFCEH 450
Db 357 LLFFVTFW-----GKKLEPKDKIKHYVPDFKLAIDHFCIH 391
QY 451 AASKVVEELOKNLGLSENNASRMTLHRFGNTSSSGIWEYELAYMEAKESVRGRDRYWO 510
Db 392 AGGRAVIDYLEKNLALPIDEASRSTLHRFGNTSSSGIWEYELAYIEAKGRKKONKRYWO 451
QY 511 IAFSGFCKNSVWVKAMRKVKKPTRRNPWVDCINRYPVL 550
Db 452 IALGSGFCKNSAVVVALNNVAKST-NSPWEHCIDRYPVKI 490

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Search completed: May 10, 2003, 23:50:22
 Job time : 592 secs

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2003, 17:59:00 ; Search time 3480 seconds
(without alignments)
12947.082 Million cell updates/sec

Title: US-09-905-657-1

Perfect score: 2782
Sequence: 1 acattactactctcaccac.....ttacgtgtataagaagatac 2782

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estcov:*
6: em_estcpl:*
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8: em_hic:*
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20: em_gss_pin:*
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25: em_gss_other:*
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27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	587.4	21.1	589	10	AV781377 AV781377
C 2	574	20.6	574	10	AV565936 AV565936
C 3	573	20.6	573	10	AV522233 AV522233
C 4	544	19.6	544	10	AV529660 AV529660
C 5	526	18.9	526	10	AV560055 AV560055
C 6	504	18.1	504	10	AV566012 AV566012

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AV781377/c	LOCUS	AV781377 RAFL2 Arabidopsis thaliana cDNA clone RAFL02-03-107 3'	AV781377	AV781377.1	GI:19800167	EST.	Arabidopsis thaliana	1 (bases 1 to 589)	Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shingawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.	Large scale analysis of Arabidopsis full-length cDNA (2002b)	Unpublished (2002)	Contact: Motoaki Seki Plant Functional Genomics Research Group RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-4359 Fax: 81-298-36-9060 Email: mseki@rc.riken.go.jp

ALIGNMENTS

AV781377 589 bp mRNA linear EST 28-MAR-2002
AV781377 RAFL2 Arabidopsis thaliana cDNA clone RAFL02-03-107 3'
mRNA sequence.
AV781377
AV781377.1 GI:19800167
EST.
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 589)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shingawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a

modified pluescript vector as a SctI/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

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BASE COUNT 176 a 137 c 117 g 159 t

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Best Local Similarity 99.8%; Pred. No. 7.3e-87;
Matches 588; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 589 TTCTCTACTCCGCCGCCGCAAAAACCAATGAAATCAAGTCTTCTCCGATCTGTC 530
QY 2085 AAGCATATCATCCCGGACTACAGCTCCCTTCGACATTTTCTCCAGCGGCAAGC 2144
DB 529 AAGCATATCATCCCGGACTACAGCTCCCTTCGACATTTTCTCCAGCGGCAAGC 470
QY 2145 AAGATAGCTTTGAAGACCTTCAAAAGAAATAGAGCTTGAAGAGAAATATGAGGCT 2204
DB 469 AAGATAGCTTTGAAGACCTTCAAAAGAAATAGAGCTTGAAGAGAAATATGAGGCT 410
QY 2205 TCTAGATGACATTCACAGGTTTGGAACAACCTTCTACAGTGAATCTGTATGAGTTG 2264
DB 409 TCTAGATGACATTCACAGGTTTGGAACAACCTTCTACAGTGAATCTGTATGAGTTG 350
QY 2265 GCTTACATGAGGCCAAGAAAGTCTGTAGAGGCGATAGGCTTGGCAGATCGCTTTC 2324
DB 349 GCTTACATGAGGCCAAGAAAGTCTGTAGAGGCGATAGGCTTGGCAGATCGCTTTC 290
QY 2325 GGTCTGTGTTTAAAGTGAACAGTGTGTGTGAAGGCAATGAGAGAGTGAAGAGCCA 2384
DB 289 GGTCTGTGTTTAAAGTGAACAGTGTGTGTGAAGGCAATGAGAGAGTGAAGAGCCA 230
QY 2385 ACCAAGAAACAATCCTTGGGTGATTCATCAACCGTTACCTGCTCTCTAAATATTC 2444
DB 229 ACCAAGAAACAATCCTTGGGTGATTCATCAACCGTTACCTGCTCTCTAAATATTC 170
QY 2445 ATTCTCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2504
DB 169 ATTCTCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 110
QY 2505 TTGATGATGAGAGTATTTACTGATCATCTGATCTAAGTCTGTATTAAGATGATGT 2564
DB 109 TTGATGATGAGAGTATTTACTGATCATCTGATCTAAGTCTGTATTAAGATGATGT 50
QY 2565 GCGTAGAGTCTGTTCACTTCAACTGTTTATTTTGTGTTGCTC 2613
DB 49 GCGTAGAGTCTGTTCACTTCAACTGTTTATTTTGTGTTGCTC 1

RESULT 2
AV565936/c 574 bp mRNA linear EST 07-SEP-2000
LOCUS
DEFINITION
thaliana cDNA clone SQ233d03f 3', mRNA sequence.
ACCESSION
AV565936
VERSION
AV565936.1 GI:8737386
KEYWORDS
EST.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 574)
AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Rabata, S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The first laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

FEATURES

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location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2e-84;
Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2073 TCCGATCTGTCCACACCATATCCCGGACTACAGCTCCGCTTGACATTTTGTCTTC 2132
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QY 2133 CACGGGAGCAAGATGTGCTTGAAGAGCTTCAAAAGAAATCTAGGCTGTGAGAG 2192
DB 514 CACGGGAGCAAGATGTGCTTGAAGAGCTTCAAAAGAAATCTAGGCTGTGAGAG 455
QY 2193 AATATGAGGCTTCTAGAGTACACACTTCAAGGTTTGAACACTTCTAGAGTGAATC 2252
DB 454 AATATGAGGCTTCTAGAGTACACACTTCAAGGTTTGAACACTTCTAGAGTGAATC 395
QY 2253 TGTATGAGTGTGCTTACATGAGGCGCAAGAAAGTCTTCTAGAGCGATAGGTTGG 2312
DB 394 TGTATGAGTGTGCTTACATGAGGCGCAAGAAAGTCTTCTAGAGCGATAGGTTGG 335
QY 2313 CAGATCGCTTCCGTTGCTTGAAGTGAACAGTGTGATGAGTGAAGCAATGAGAG 2372
DB 334 CAGATCGCTTCCGTTGCTTGAAGTGAACAGTGTGATGAGTGAAGCAATGAGAG 275
QY 2373 GTGAAGAGCCAAACGAGAACATCCTTGGGTGATTCATCAACCGTTACCGTGTGCT 2432
DB 274 GTGAAGAGCCAAACGAGAACATCCTTGGGTGATTCATCAACCGTTACCGTGTGCT 215
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DB 214 CTCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 155
QY 2493 GATACAGTTTGGTGGATGATAGAGTATTTACTGATCATCTGATCTAAGTCTGTAT 2552
DB 154 GATACAGTTTGGTGGATGATAGAGTATTTACTGATCATCTGATCTAAGTCTGTAT 95
QY 2553 AAGAAATGATGTGCTAGAGTCTGTTCAAGCTTCAACTGTTTATTTTGTGTTCT 2612
DB 94 AAGAAATGATGTGCTAGAGTCTGTTCAAGCTTCAACTGTTTATTTTGTGTTCT 35
QY 2613 CTATTGATCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2646
DB 34 CTATTGATCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1

RESULT 3
AV522233/c 573 bp mRNA linear EST 01-SEP-2000
LOCUS
AV522233

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DEFINITION  AV522233 Arabidopsis thaliana aboveground organs two to six-week
ACCESSION   AV522233
VERSION     AV522233.1 GI:8681760
KEYWORDS    EST.
SOURCE      thale cress.
ORGANISM    Arabidopsis thaliana
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE   1 (bases 1 to 573)
AUTHORS    Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE       A large scale analysis of cDNA in Arabidopsis thaliana: Generation
             of 12,028 non-redundant expressed sequence tags from normalized and
             size-selected cDNA libraries
JOURNAL     DNA Res. 7, 175-180 (2000)
MEDLINE    20363093
COMMENT     Contact: Erika Asamizu
             The First Laboratory for Plant Gene Research
             Kazusa DNA Research Institute
             Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
             Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
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QY 2074 CCGATCTCTCCAGGCAATACATCCCGGACTACAGCTGCGCTTCAGCATTTTTCCTCC 2133
DB 513 CCGATCTCTCCAGGCAATACATCCCGGACTACAGCTGCGCTTCAGCATTTTTCCTCC 454
QY 2134 ACGCGGCAAGCAAACTAGCTGTGAAGAGCTTCAAAAGATCTAGGTTGAGTGAAGA 2193
DB 453 ACGCGGCAAGCAAACTAGCTGTGAAGAGCTTCAAAAGATCTAGGTTGAGTGAAGA 394
QY 2194 ATATGAGAGCTTCTAGATGACACTTCAAGGTTTGAACACTTCTAGCACTGGAATCT 2253
DB 393 ATATGAGAGCTTCTAGATGACACTTCAAGGTTTGAACACTTCTAGCACTGGAATCT 334
QY 2254 GGTATGATTTGGCTTACATGAGGCCAAGAAAGTTCGTAAGAGCGATAGGCTTTGGC 2313
DB 333 GGTATGATTTGGCTTACATGAGGCCAAGAAAGTTCGTAAGAGCGATAGGCTTTGGC 274
QY 2314 AGATCGCTTTGGTCTCTGTTTAAAGTGAACAGTGTGTTGGAAGGCAATGAGGAAG 2373
DB 273 AGATCGCTTTGGTCTCTGTTTAAAGTGAACAGTGTGTTGGAAGGCAATGAGGAAG 214
QY 2374 TGAAGAACCCCAACGAGAACAATCCTGGTGATTTGCATCAACCGTTACCGCTGTCC 2433
DB 213 TGAAGAACCCCAACGAGAACAATCCTGGTGATTTGCATCAACCGTTACCGCTGTCC 154
QY 2434 TCTAATATATCTCTCTAATTAATTAATCAAGTAGATCTCTAATTAATCTCCCAACCAAG 2493
DB 153 TCTAATATATCTCTCTAATTAATTAATCAAGTAGATCTCTAATTAATCTCCCAACCAAG 94

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QY 2494 ATACAGTTGGTGGATGATAGAGTTATTTACTGATCATCTGATCAAGTCTGTATA 2553
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QY 2554 AGAATGATGTGGCTAGAGTCTGTTCAAGCTTC 2586
DB 33 AGAATGATGTGGCTAGAGTCTGTTCAAGCTTC 1
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LOCUS      AV529660 Arabidopsis thaliana aboveground organs two to six-week
DEFINITION AV529660 Arabidopsis thaliana aboveground organs two to six-week
ACCESSION   AV529660
VERSION     AV529660.1 GI:8689943
KEYWORDS    EST.
SOURCE      thale cress.
ORGANISM    Arabidopsis thaliana
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             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE   1 (bases 1 to 544)
AUTHORS    Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE       A large scale analysis of cDNA in Arabidopsis thaliana: Generation
             of 12,028 non-redundant expressed sequence tags from normalized and
             size-selected cDNA libraries
JOURNAL     DNA Res. 7, 175-180 (2000)
MEDLINE    20363093
COMMENT     Contact: Erika Asamizu
             The First Laboratory for Plant Gene Research
             Kazusa DNA Research Institute
             Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
             Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
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DB 544 GGCCTCTAGATGACACTTCAAGGTTTGAACACTTCTAGCACTGGAATCTGTATGA 485
QY 2261 GTTGCTTACATGAGGCCAAGAAAGTTCGTAAGAGCGATAGGCTTTGCCAGATGCG 2320
DB 484 GTTGCTTACATGAGGCCAAGAAAGTTCGTAAGAGCGATAGGCTTTGCCAGATGCG 425
QY 2321 TTTCGGTCTGTTTTAAGTGAACAGTGTGTTGGAAGGCAATGAGGAAGTGAAGA 2380
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QY 2381 GCCAACCAAGAACCAATCCTTGGTGATTTGCATCAACCGTTACCGCTGTCTAAT 2440
DB 364 GCCAACCAAGAACCAATCCTTGGTGATTTGCATCAACCGTTACCGCTGTCTAAT 305
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Db	184	ATGTGGCTAGAGATCCGTGTTCAGCTTCAACTCTGTTTATTTTGTCTTTCATTTGCA	125
OY	2621	TCTTCATTAACCTTTGAGAGATTTAAAGAAAAAACTCTCTTTAGTTGATGAAACAGATG	2680
Db	124	TCTTCATTAACCTTTGAGAGATTTAAAGAAAAAACTCTCTTTAGTTGATGAAACAGATG	65
OY	2681	GTCACTGTAAATCTCTTATATATGCAAGGTAAACAAATTCCTTTTAAAGCAATCATAT	2740
Db	64	GTCACTGTAAATCTCTTATATATGCAAGGTAAACAAATTCCTTTTAAAGCAATCATAT	5
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Db	4	TCAG 1	
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LOCUS			
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	Arabidopsis thaliana		
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	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.		
REFERENCE	1 (bases 1 to 526)		
AUTHORS	Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.		
TITLE	A large scale analysis of cDNA in Arabidopsis thaliana: Generation		
	of 12,028 non-redundant expressed sequence tags from normalized and		
	size-selected cDNA libraries		
JOURNAL	DN Res. 7, 175-180 (2000)		
MEDLINE	20363093		
COMMENT	Contact: Erika Asamizu		
	The First Laboratory for Plant Gene Research		
	Kazusa DNA Research Institute		
	Yana 1532-3, Kisarazu, Chiba 292-0812, Japan		
	Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.		
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Db	526	GGCTTCAGATGACACTTCCACAGGTTTGGAAACACTTCTAGCAGTGGAAATCTGATGA	467
OY	2261	GTTGGCTTACATGAGAGCCAAAGAAAGTTCGTGATGAGAGCATAGGCTTTGGCAGATGC	2320
Db	466	GTTGGCTTACATGAGAGCCAAAGAAAGTTCGTGATGAGAGCATAGGCTTTGGCAGATGC	407
OY	2321	TTTCGGTCTCTGTTTAAAGTGTACAGTGTGCTGTGGAGGCAATGACAGAGGTGAACGA	2380

Dd	406	TTTGGCTTCGTTTTTAAGTGTAACAGTGTGTGTGGAAGCAATGAGAAGCTAAGA	347
Oy	2381	GCCAAACCGAACAACATCCTTGGGTGGATTGCATCACCGTACCCTGTGCTCTTAAT	2440
Dd	346	GCCAACCGAACAACATCCTTGGGTGGATTGCATCACCGTACCCTGTGCTCTTAAT	287
Oy	2441	TATCATTTCTTCTTAATTAATCAATAAGATCTCTAATTACTCCAACCAAAAAGATACGT	2500
Dd	286	TATCATTTCTTCTTAATTAATCAATAAGATCTCTAATTACTCCAACCAAAAAGATACGT	227
Oy	2501	TTGGTTGATGATGAGAGATTAATTTACTGATCATCTGTATCTCAAGCTCTTTAAAGATNG	2560
Dd	226	TTGGTTGATGATGATGAGAGATTAATTTACTGATCATCTGTATCTCAAGCTCTTTAAAGATNG	167
Oy	2561	ATGTGGCTTAGAGTCCGTGTTCAAGCTTCAAACCTGTTTATTTTGTGTTCTCTATTTGGA	2620
Dd	166	ATGTGGCTTAGAGTCCGTGTTCAAGCTTCAAACCTGTTTATTTTGTGTTCTCTATTTGGA	107
Oy	2621	TCTTCATTAACCTTAGAGATTAAGAAAAAACCTCTTCTAGTTATGTAACAGATNG	2680
Dd	106	TCTTCATTAACCTTAGAGATTAAGAAAAAACCTCTTCTAGTTATGTAACAGATNG	47
Oy	2681	GTTCATTTGTAATTTCTTTATATATGTCAAAGTAAACAAATTTCTTTT	2726
Dd	46	GTTCATTTGTAATTTCTTTATATATGTCAAAGTAAACAAATTTCTTTT	1
RESULT 6			
AVS66012/c			
LOCUS	AVS66012	504 bp	mRNA linear EST 07-SEP-2000
DEFINITION	AVS66012 Arabidopsis thaliana green siliques Columbia Arabidopsis		
THALIANA CDNA CLONE SQ235d01F 3', mRNA SEQUENCE.			
ACCESSION	AVS66012		
VERSION	AVS66012.1	GI:8737462	
KEYWORDS	EST.		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
EUKARYOTA; VIRIDIPHYTES; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.			
REFERENCE	1 (bases 1 to 504)		
AUTHORS	Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.		
TITLE	A large scale analysis of cDNA in Arabidopsis thaliana: Generation		
JOURNAL	of 12,028 non-redundant expressed sequence tags from normalized and		
MEDLINE	size-selected cDNA libraries		
COMMENT	DNA Res. 7, 175-180 (2000)		
Contact: Erika Asamizu			
The First Laboratory for Plant Gene Research			
Kazusa DNA Research Institute			
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan			
Email: asamizue@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.			
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/strain="Columbia"			
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/clone="SQ235d01F"			
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:			
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Query Match	18.1%; Score 504; DB 10; Length 504;		
Best Local Similarity	100.0%; Prid. No. 3.7e-73;		
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Oy	2143	GCAAGTAGTCTGGAAGAGCTTCAAAAGATCTTAGAGCTTGAGTGAAGAATATGAGG	2202
Dd	504	GCAAGTAGTCTGGAAGAGCTTCAAAAGATCTTAGAGCTTGAGTGAAGAATATGAGG	445

QY 2203 CTCTAGATGACACCTTCACAGGTTTGGAAACACTTCTAGCAGTGAATCTGTATGAGT 2262
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 DB 444 CTTCTAGATGACACCTTCACAGGTTTGGAAACACTTCTAGCAGTGAATCTGTATGAGT 385
 |||
 QY 2263 TGGCTTACATGAGAGCCCAAGAAAGTGTCTAGAGCGATAGGGTTTGGCAGATCGCTT 2322
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 DB 384 TGGCTTACATGAGAGCCCAAGAAAGTGTCTAGAGCGATAGGGTTTGGCAGATCGCTT 325
 |||
 QY 2232 TCGGTTCTGTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2382
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 DB 324 TCGGTTCTGTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 265
 |||
 QY 2383 CAACAGGAGAACATCTCTGGTGGATTTGATTCATCAACCGCTCTGCTCTCTAAATTA 2442
 |||
 DB 264 CAACAGGAGAACATCTCTGGTGGATTTGATTCATCAACCGCTCTGCTCTCTAAATTA 205
 |||
 QY 2443 TCATCTCTCTAAATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2502
 |||
 DB 204 TCATCTCTCTAAATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 145
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 QY 2503 GGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2562
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 DB 144 GGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 85
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 QY 2563 GTGGCTAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2622
 |||
 DB 84 GTGGCTAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 25
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 QY 2623 TTCTATTAACCTTTGAGAGATTAAG 2646
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 DB 24 TTCTATTAACCTTTGAGAGATTAAG 1

RESULT 7
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 LOCUS BOGYJ82TR BOGY Brassica oleracea genomic clone BOGYJ82, DNA
 DEFINITION sequence.
 ACCESSION BH444293
 VERSION BH444293.1 GI:17630007
 KEYWORDS GSS.
 SOURCE Brassica oleracea.
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 775)
 REFERENCE Town, C.D., Van Aken, S., Uterback, T. and Fraser, C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished (2001)
 JOURNAL Other GSSs: BOGYJ82TF
 COMMENT Contact: Chris Town
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.
 location/Qualifiers
 1..775
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 /strain="N01000DH3"
 /db_xref="taxon:3712"
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 /clone_1bp="BOGY"
 /note="Vector: pHOSt1, Site 1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 218 a 167 c 165 g 205 t

Query Match 17.8%; Score 494.6; DB 17; Length 775;

Best Local Similarity 86.7%; Pred. No. 1.1e-71;
 Matches 556; Conservative 0; Mismatches 84; Indels 1; Gaps 1.

QY 1118 GGTGCAAAAAGAGAGCTTCATGAACTAGCCGAAAATCAGGAAAGTTGACGAAGAGAC 1177
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 DB 746 GGTGCAAAAAGAGAGCTTCATGAACTAGCCGAAAATCAGGAAAGTTGACGAAGAGAT 688
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 QY 1178 ACTGGTTTCAAGAGAGATCTTCAAGCCCTCAGGCAATGAGCGAGACATAGTCC 1237
 |||
 DB 687 CTTGATTTTCAAGAGAGATCTTCAAGCCCTCAGGCAATGAGCGAGACATAGTCC 628
 |||
 QY 1238 AAGATCCATCTCTTCATGAGAAACATTAACAGATGAAAGAGTCTGGAAGAGCTC 1297
 |||
 DB 627 AAGATCCATCTCTTCATGAGAAACATTAACAGATGAAAGAGTCTGGAAGAGCTC 568
 |||
 QY 1298 TACAGTATCTTTGAGACATAGACAACTCTTGAGAAAGACAGTGTAAACCTTAAGA 1357
 |||
 DB 567 GATGATGATATCTGCGGACATGACGAACTCTTCAGAAAGACAGTGTAAACCTTAAGA 508
 |||
 QY 1358 CGTGGTGTCTTGGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1417
 |||
 DB 507 CGTGGTGTCTTGGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 448
 |||
 QY 1418 GGTGATTAACCATTAACAGATGAGAGGAGACATTAAGTTTCAACCTTGAGAGATGG 1477
 |||
 DB 447 GGTGATTAACCATTAACAGATGAGAGGAGACATTAAGTTTCAACCTTGAGAGATGG 388
 |||
 QY 1478 ATGTTGGCTGGAATCATAGCTATTGATCTCTGCTGATGATGATGATGATGATGAT 1537
 |||
 DB 387 TTGCTACACAGAGAAATCAATGACCGTTGATCTCTGCTGATGATGATGATGATGAT 328
 |||
 QY 1538 TAGTATGCTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1597
 |||
 DB 327 TAGTATGCTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 268
 |||
 QY 1598 CAAGTCAATGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1657
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 DB 267 CAAGTCAATGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 208
 |||
 QY 1658 TAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1717
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 DB 207 TAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 148
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 QY 1718 TAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1758
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 DB 147 CAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 107
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RESULT 8
 AV828119 585 bp mRNA linear EST 01-APR-2002
 LOCUS AV828119 RAP19 Arabidopsis thaliana cDNA clone RAP109-24-C03 5',
 DEFINITION mRNA sequence.
 ACCESSION AV828119
 VERSION AV828119.1 GI:19870179
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 585)
 REFERENCE Seki, M., Narusaka, M., Ishida, J., Kamliya, A., Satou, M., Nakajima, M.,
 Oono, Y., Sakurai, T., Carninci, P., Kawah, J., Itoh, M., Ishii, Y.,
 Arai, K., Shikata, K., Shingawa, A., Muramatsu, M., Hayashizaki, Y.
 and Shinozaki, K.
 Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359

Db 482 ATGAACAAAGTGCACAAAGAGAGTTCATAGA 515
|||||
RESULT 10
AV560773/c 474 bp mRNA linear EST 07-SEP-2000
AV560773 Arabidopsis thaliana green siliques Columbia Arabidopsis
DEFINITION
thaliana cDNA clone S014007F 3', mRNA sequence.
ACCESSION
AV560773
VERSION
AV560773.1 GI:8732199
KEYWORDS
EST.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 474)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
JOURNAL
MEDLINE
20363093
COMMENT
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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XhoI"
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Best Local Similarity 100.0%; Pred. No. 3.2e-68;
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QY 2195 TATGAGGCTCTAGATGACACTTACAGTTGGAAACCTTACAGTGGAACTG 2254
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Db 474 TATGAGGCTCTAGATGACACTTACAGTTGGAAACCTTACAGTGGAACTG 415
QY 2255 GTATGAGTTGGCTTACATGAGGCCAAGAAAGTTCGTAGAGCGATAGGTTGGCA 2314
|||||
Db 414 GTATGAGTTGGCTTACATGAGGCCAAGAAAGTTCGTAGAGCGATAGGTTGGCA 355
QY 2315 GATGCTTTGCTGCTGCTTTAAAGTGAACAGTGTGTGGAAAGCAATGAGCAAGT 2374
|||||
Db 354 GATGCTTTGCTGCTGCTTTAAAGTGAACAGTGTGTGGAAAGCAATGAGCAAGT 295
QY 2375 GAAGAAGCAACGAGAAACATCTTGGGGATTCGATCAACCGTTACCGTGGCCCT 2434
|||||
Db 294 GAAGAAGCAACGAGAAACATCTTGGGGATTCGATCAACCGTTACCGTGGCCCT 235
QY 2435 CTAATATATCATCTTCTTAATTAATCACTAGATCTCAATTAATCTCAACCAAGA 2494
|||||
Db 234 CTAATATATCATCTTCTTAATTAATCACTAGATCTCAATTAATCTCAACCAAGA 175
QY 2495 TACAGTTGGTTGATGATGAGAGTATTTACGATCACTTCGATCTAAGCTGTTATA 2554
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Db 174 TACAGTTGGTTGATGATGAGAGTATTTACGATCACTTCGATCTAAGCTGTTATA 115
QY 2555 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2614
|||||
Db 114 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 55

QY 2615 ATTGATCTTCATTAACCTTGGAGATTAAGAAAAAACTCTCTTAGTTG 2668
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Db 54 ATTGATCTTCATTAACCTTGGAGATTAAGAAAAAACTCTCTTAGTTG 1
RESULT 11
AV564080/c 474 bp mRNA linear EST 07-SEP-2000
AV564080 Arabidopsis thaliana green siliques Columbia Arabidopsis
DEFINITION
thaliana cDNA clone S0198102F 3', mRNA sequence.
ACCESSION
AV564080
VERSION
AV564080.1 GI:8735506
KEYWORDS
EST.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 474)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
JOURNAL
MEDLINE
20363093
COMMENT
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/tissue_type="green siliques"
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XhoI"
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Best Local Similarity 100.0%; Pred. No. 3.2e-68;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2252 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2311
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Db 474 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 415
QY 2312 GCAGATCCCTTTCGCTTCTGTTTAAGTGAACAGTGTGTGGAAAGCAATGAGAA 2371
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Db 414 GCAGATCCCTTTCGCTTCTGTTTAAGTGAACAGTGTGTGGAAAGCAATGAGAA 355
QY 2372 GGTGAAGAAGCAACGAGAAACATCTTGGGTGATTCATCAACCGTTACCGTGGCC 2431
|||||
Db 354 GGTGAAGAAGCAACGAGAAACATCTTGGGTGATTCATCAACCGTTACCGTGGCC 295
QY 2432 TCTCTAATATCATCTTCTTAATTAATCAAGTGAATCTTAATTAATCAACCA 2491
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Db 294 TCTCTAATATCATCTTCTTAATTAATCAAGTGAATCTTAATTAATCAACCA 235
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QY 2552 TAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2611
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Db 174 TAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 115
QY 2612 TCTATGATCTTCATTAACCTTGGAGATTAAGAAAAAACTCTCTTAGTTGATA 2671

|||||
 Db 114 TCTATTGATCTTCATTAACCTTGAGAGATTAAAGAAAAAACTCTTCTTATGTTGARA 55
 Oy 2672 GAACAGATGCTATGTTATTTCTTAATATGCAAAAGTAAACATTTCTTTT 2725
 Db 54 GACACAGATGCTATGTTATTTCTTAATATGTCACAAAGTAAACATTTCTTTT 1

RESULT 12
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 LOCUS AV563747
 DEFINITION AV563747 Arabidopsis thaliana green siliques Columbia Arabidopsis
 accession AV563747
 VERSION AV563747.1 GI:8735173
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 462)
 Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 A large scale analysis of cDNA in Arabidopsis thaliana: Generation
 of 12,028 non-redundant expressed sequence tags from normalized and
 size-selected cDNA libraries
 DNA Res. 7, 175-180 (2000)
 JOURNAL 20363093
 MEDLINE
 COMMENT Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yama 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/
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 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
 XhoI"
 BASE COUNT 158 a 99 c 69 g 136 t
 ORIGIN

Query Match 16.5%; Score 460.4; DB 10; Length 462;
 Best Local Similarity 99.8%; Pred. No. 5.5e-66;
 Matches 461; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 462 ACATGAGGCCAAGAAAGTTCGTAGAGGCGATAGGTTGGCAGATCGCTTTCGTT 403
 Oy 2329 CTGGTTTAAAGTGAACATGTGGTGTGAAGCAATGAGAGTGAAGCAACCA 2388
 Db 402 CTGGTTTAAAGTGAACATGTGGTGTGAAGCAATGAGAGTGAAGCAACCA 343
 Oy 2389 GGAACAATCCCTGGTGGATGCATCAACCGTTACCGTGCCTCTTAATTATCATTC 2448
 Db 342 GGAACAATCCCTGGTGGATGCATCAACCGTTACCGTGCCTCTTAATTATCATTC 283
 Oy 2449 TTCTAAATTAATCAAGTAAATCTCTAATTAATCTCCAAACCAAGATACAGTTGGTGG 2508
 Db 282 TTCTAAATTAATCAAGTAAATCTCTAATTAATCTCCAAACCAAGATACAGTTGGTGG 223
 Oy 2509 ATGATAGAGGATTAATTAATGATCATTCGTATCAAGTCTGTATTAAGAAATGATGTGGCT 2568
 Db 222 ATGATAGAGGATTAATTAATGATCATTCGTATCAAGTCTGTATTAAGAAATGATGTGGCT 163
 Oy 2569 AAGATGCTGATGATCAACCTGTTTATTTTGGTGTCTCTATATGATGATCTTCA 2628
 Db 162 AAGATGCTGATGATCAACCTGTTTATTTTGGTGTCTCTATATGATGATCTTCA 103

Oy 2629 AACTTGAGAGATTAAGAAAAAACTCTTCTTATGTTGATGAACAGATGTCATTC 2688
 Db 102 AACTTGAGAGATTAAGAAAAAACTCTTCTTATGTTGATGAACAGATGTCATTC 43
 Oy 2689 AATTCTTTAATATGTCAAAGTAAACAAATTTCTTTTAAG 2730
 Db 42 AATTCTTTAATATGTCAAAGTAAACAAATTTCTTTTAAG 1

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 LOCUS AV797399
 DEFINITION AV797399 Arabidopsis thaliana cDNA clone RAF109-11-P14 3',
 mRNA sequence.
 AV797399
 VERSION AV797399.1 GI:19831382
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 453)
 Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.,
 and Shinozaki, K.
 Large scale analysis of Arabidopsis full-length cDNA (2002b)
 Unpublished (2002)
 JOURNAL Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyada, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: mseki@rc.riken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
 and XhoI was ligated to modified Lambda F1C-1 vector (Carninci et
 al., submitted for publication) digested with BamHI and SalI. This
 clone is in a modified pBluescript vector. Please visit our web
 site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
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 Location/Qualifiers
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 ORIGIN

Query Match 16.2%; Score 451.4; DB 10; Length 453;
 Best Local Similarity 99.8%; Pred. No. 1.7e-64;
 Matches 452; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2279 CAAGGAAGTTCGTAGAGGCGATAGGTTGGCAGATCGCTTTCGTTTAA 2338
 Db 453 CAAGGAAGTTCGTAGAGGCGATAGGTTGGCAGATCGCTTTCGTTTAA 394
 Oy 2339 GTGTAACTGTGTGTGAAGCAATGAGAGTGAAGAACCAACGAGAACATCC 2398
 Db 393 GTGTAACTGTGTGTGAAGCAATGAGAGTGAAGAACCAACGAGAACATCC 334
 Oy 2399 TTGGGTGATGTCATCAACCGTTACCGTGCCTCTTAATTATCATTCCTTAATTA 2458


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Db 383 ACAGTGTGTGGAGGCAATGAGAGATGAGAACCAACCAAGACAATCCTTGGG 324
QY 2404 TGGATTCATCAACCGTTACCGTGGCTCTTAATTATCATTCCTTAATTAAATCA 2463
Db 323 TGGATTGCATCAACCGTTACCGTGGCTCTTAATTATCATTCCTTAATTAAATCA 264
QY 2464 AGTAGATCTCTAATTACTCGAACCAAAAGATACAGTTGGTTGGATGATAGAGTTATT 2523
Db 263 AGTAGATCTCTAATTACTCGAACCAAAAGATACAGTTGGTTGGATGATAGAGTTATT 204
QY 2524 TACTGATCATTCGATCTAGCTGTATTAAGAAATGATGGCTAGAGTCCGTGTCAGC 2583
Db 203 TACTGATCATTCGATCTAGCTGTATTAAGAAATGATGGCTAGAGTCCGTGTCAGC 144
QY 2584 TTCACCTGTGTTATTTTGTGTTCTCTATTGGATCTTCATAAACTTGAGAGATTA 2643
Db 143 TTCACCTGTGTTATTTTGTGTTCTCTATTGGATCTTCATAAACTTGAGAGATTA 84
QY 2644 AAGAAAAAACTCTCTTACTTGTGATAGACAGATGTCATGTAATTTCTTAATATG 2703
Db 83 AAGAAAAAACTCTCTTACTTGTGATAGACAGATGTCATGTAATTTCTTAATATG 24
QY 2704 TCAAGTAAACAATTTCTTTT 2726
Db 23 TCAAGTAAACAATTTCTTTT 1
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Search completed: May 10, 2003, 21:02:25
Job time : 3505 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2003, 17:46:08 ; Search time 6984 Seconds
(without alignments) 11592.784 Million cell updates/sec

Title: US-09-905-657-1
Perfect score: 2782
Sequence: 1 acattactactctcacca.....ttacgtgtataagaagatac 2782

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
2: gb_bt:*
3: gb_in:*
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5: gb_ov:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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8	1412.4	50.8	1425	AF214497S2	AF214498 Arabidops
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10	1412.4	50.8	1425	AF214501S2	AF214502 Arabidops
11	1412.4	50.8	1425	AF214503S2	AF214504 Arabidops
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ALIGNMENTS

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LOCUS AX353344 2782 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 1 from Patent EP1174517.
ACCESSION AX353344
VERSION AX353344.1 GI:18618426
KEYWORDS
SOURCE
ORGANISM
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS
TITLE
Lechelt-Kunze,C., Meissner,R. and Tietjen,K.
Use of very long chain fatty acid elongase for the identification


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ACCESSION AJ010713
VERSION AJ010713.1 GI:3559808
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SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 2782)
Yephremov A., Wismar, E., Hüljser, P., Hüljser, C., Wellesen, K. and
Saedler, H.
TITLE Characterization of the FIDDLEHEAD gene of Arabidopsis reveals a
link between adhesion response and cell differentiation in the
epidermis
JOURNAL Plant Cell 11 (11), 2187-2201 (1999)
MEDLINE 20025656
PubMed 10559443
REFERENCE 2 (bases 1 to 2782)
AUTHORS Yephremov, A.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-1998) Yephremov A., Molekulare Pflanzen-genetik,
Max-Planck-Institut fuer Zuechtungs-forschung, Carl-von-Linne-Weg
10, Koeln D-50829, Germany
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 1 (bases 1 to 82212)
 Rounsley, S.D., Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C.,
 Somerville, C.R., and Venter, J.C.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 82212)
 Lin, X.
 JOURNAL Direct Submission
 TITLE Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
 JOURNAL Medical Center Dr., Rockville, MD 20850, USA
 REFERENCE 3 (bases 1 to 82212)
 Town, C.D. and Kaul, S.
 TITLE Direct Submission
 JOURNAL Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA, cdtown@tigr.org
 COMMENT On Apr 18, 2002 this sequence version replaced by: 5598423.
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 contains LRR Leucine Rich Repeat domains; supported by
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 8920..8991,9079..9150,9277..9348,9431..9502,9589..9660,
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 8920..8991,9079..9150,9277..9348,9431..9502,9589..9660,
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 mRNA 19166..23272
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Query Match 99.1%; Score 2758; DB 8; Length 82212;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2780; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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QY	121	CTTCATCAACCTATAGATCTCATATATCACTACACCAACCAACCAAGATGG	180
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QY	481	CTTCGCTCTCTTTTAAACCGCTTGCTGCTACTCATGCTGCTGCTGCTGTTA	540
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QY	541	TCTTATTTATTTGCTTTTACAGCCCTCCGATGGAACAGAGTACCTCCCACTTTC	600
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DB	47814	TAGTAAATATTTTCAAGTATATATAAAGATTAATTTTGCAGAAACCTTAGATATG	47873

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Db 47874 GTTACGTTGATTTAAACCGAATGTTGCTAGAAATTTGAGAAAGTAGATAACCTAAA 47933
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Db 47934 AACTCCGATTAAAGAAACCGGTTGACTATATATTTTAACTGCTTCTGTTTCAATTT 47993
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Db 48053 CGGACGATATATTAATGAAGCTGAATCAACCAACAAAGTTTCATTTATTTCCGGTTC 48112
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Db 48113 TCTCGGGTTTAACTCTCTTTTGCATTTGATTTGTTAGTGTAGACAAAAAGAGATTCTAATG 48172
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Db 48173 AACTAGCGAATAATCAGGGAAGTTGACAGAGACACTCGGTTTAAAGAGAGATCT 48232
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Db 48233 TACAAGCCTAGGCAATGAGGAGAGACATACGTCACAGATCTCTTTCATCAGAAA 48292
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Db 48832 AATTTGTGTGTTTTAGAGAGTGTGTACAGAGAAAGATGAAACAAGATTCAAGGGGT 48891
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Db 48892 TGAAGATTAATAGACTTAATGGAATTTGAGAGTGAAGCTCTCAAGACAATCACTACTA 48951

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OY 2341 GTAAAGTGTGTGTGGAAGGCAATGAGAGAGAGGTAAGAAACCAACAGAAACATCTT 2400
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Db 49612 AGCTTCAACTGTTTATTTTGTGTTCTCTATGATGATCTTCAATTTTGAAGA 49671
OY 2641 TTAAGAAAAAACTCTCTTCTAGTTGATGAGACAGATGCTCATTTGTAATTTCTTAAT 2700
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RESULT 4

AF2144489S2 1425 bp DNA linear PLN 17-MAY-2000
LOCUS AF214489S2
DEFINITION Arabidopsis thaliana cultivar Landsberg erecta fiddlehead protein
(fhd) gene, complete cds.
ACCESSION AF214490
VERSION AF214490.1 GI:8177698
KEYWORDS 2 of 2
SEGMENT Arabidopsis thaliana.
SOURCE Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 1425)

Prutic, R.E., Vielle-Calzada, J.P., Ploense, S.E., Grossniklaus, U. and Lolle, S.J.

TITLE FIDDLEHEAD, a gene required to suppress epidermal cell interactions in Arabidopsis, encodes a putative lipid biosynthetic enzyme

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)

MEDLINE 20122614

PUBMED 10655527

REFERENCE 2 (bases 1 to 1425)

Prutic, R.E., Vielle-Calzada, J.P., Ploense, S.E., Grossniklaus, U. and Lolle, S.J.

TITLE Direct Submission

JOURNAL Submitted (13-Dec-1999) Molecular and Cellular Biology, Harvard University, 16 Divinity Avenue, Cambridge, MA 02138, USA

FEATURES Location/Qualifiers

source 1..1425

organism "Arabidopsis thaliana"

cultivar "Landsberg erecta"

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order (AF214489.1:1..656,1..1425)

gene /gene="fdbh"

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mRNA join(AF214489.1:1..97..504,11..636,711..1329)

product "fiddlehead protein"

protein "fdbh"

codon_start 1

evidence "not experimental"

product "fiddlehead protein"

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BASE COUNT 396 a 294 c 335 g 400 t

ORIGIN

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Matches 1425; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 1 ATTGGTTAGTGACAAAAGAGATTCATAGACTAGCGAAATCAGGAACTTGA 60

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QY 1229 ATAGTCCCAAGATCCATCTTTCATCAGAAACATACAGATGAAAGAGTCTGA 1288
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Db 121 ATAGTCCCAAGATCCATCTTTCATCAGAAACATACAGATGAAAGAGTCTGA 180

QY 1289 AGAAGCCTCAGAGATCTTGGAGCCTAGAGAACTCTTCGAGAGACAGCTGAA 1348
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Db 181 AGAAGCCTCAGAGATCTTGGAGCCTAGAGAACTCTTCGAGAGACAGCTGAA 240

QY 1349 ACCTAAGACGTTGCTCTTGTGTTAACTAGATGATTTCAACCGACCGCTCTT 1408
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Db 241 ACCTAAGACGTTGCTCTTGTGTTAACTAGATGATTTCAACCGACCGCTCTT 300

QY 1409 GTCCGCAATGATGATTAACATTAAGAGAGGAACTACTAGTACAACTTGG 1468
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Db 301 GTCCGCAATGATGATTAACATTAAGAGAGGAACTACTAGTACAACTTGG 360

QY 1469 AGGATGGGATGTTGGCTGTGAATCATAGATGATCTTGGTGCATGCTTCACT 1528
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Db 361 AGGATGGGATGTTGGCTGTGAATCATAGATGATCTTGGTGCATGCTTCACT 420

QY 1529 TAACCTAATGATGATGCTTGTGTTGAGTACTAGATGATGATGATGATGAT 1588
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Db 421 TAACCTAATGATGATGCTTGTGTTGAGTACTAGATGATGATGATGATGAT 480

QY 1589 GCGAAGTACAGATCATAGTATTAACCTAATGATGATGATGATGATGATGAT 1648
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Db 481 GCGAAGTACAGATCATAGTATTAACCTAATGATGATGATGATGATGATGAT 540

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Db 541 TATGCTCTTAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

QY 1709 CCGAAGTACATAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1768
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QY 1769 CGTTTACATCTCTTGAACCACTAGTATTAATTTGTTGTTGTTGTTGTTGTT 1828
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Db 661 CGTTTACATCTCTTGAACCACTAGTATTAATTTGTTGTTGTTGTTGTTGTT 719

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Db 720 CCAGAAAGATGATGAACAGAGATTCAGAGGTTGAAGATAGTACACTAATGAAGT 779

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Db 780 TGAAGTGAAGCTCTCAAGACAAACATCACTTACCTAGCTCTTGTCTTACT 839

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QY 2069 CTCTTCGATCTGTCCAAACCATCAATCCGAGCTACAGCTGCTTGCAGCAT 2128
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Db 960 CTCTTCGATCTGTCCAAACCATCAATCCGAGCTACAGCTGCTTGCAGCAT 1019

QY 2129 CTTCACGCGGCAAGCAAGATGCTTGAAGCTTCAAAAGATCAGGCTTGAGTGA 2188
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LOCUS Arabidopsis thaliana fiddlehead protein (fdh) gene, fdh-1 allele,
DEFINITION complete cds.
ACCESSION AF214492
VERSION AF214492.1 GI:8177702
KEYWORDS 2 of 2
SEGMENT Arabidopsis thaliana.
SOURCE Arabidopsis thaliana.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1425)
Pruitt, R.E., Velle-Calzada, J.P., Ploense, S.E., Grossniklaus, U. and
Lolle, S.J.
TITLE FIDDLEHEAD, a gene required to suppress epidermal cell interactions
in Arabidopsis, encodes a putative lipid biosynthetic enzyme
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)
MEDLINE 20122614
PUBMED 10655527
REFERENCE 2 (bases 1 to 1425)
Pruitt, R.E., Velle-Calzada, J.P., Ploense, S.E., Grossniklaus, U.
and Lolle, S.J.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-1999) Molecular and Cellular Biology, Harvard
University, 16 Divinity Avenue, Cambridge, MA 02138, USA
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KRIILASGIGDETYPRSSISSENTITTKEGREASTVIFGALDELFEKTRKPKVYG
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BASE COUNT 397 a 294 c 334 g 400 t
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|||||
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RESULT 6	AF214493S2		
LOCUS	AF214493S2	1425 bp	DNA linear
DEFINITION	Arabidopsis thaliana fiddlehead protein (fdh) gene, fdh-2 allele, complete cds.		
ACCESSION	AF214494		
VERSION	AF214494.1	GI:8177706	
KEYWORDS			
SEGMENT			
ORGANISM	2 of 2		
SOURCE	Arabidopsis thaliana.		
REFERENCE	Arabidopsis thaliana Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1425)		
REFERENCE	Prittc,R.E., Vielle-Calzada,J.P., Ploense,S.E., Grossniklaus,U. and Fiddlehead, a gene required to suppress epidermal cell interactions in Arabidopsis, encodes a putative lipid biosynthetic enzyme Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)		
REFERENCE	2 (bases 1 to 1425)		
REFERENCE	Prittc,R.E., Vielle-Calzada,J.-P., Ploense,S.E., Grossniklaus,U. and Fiddlehead, a gene required to suppress epidermal cell interactions in Arabidopsis, encodes a putative lipid biosynthetic enzyme Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)		
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REFERENCE	Prittc,R.E., Vielle-Calzada,J.-P., Ploense,S.E., Grossniklaus,U. and Fiddlehead, a gene required to suppress epidermal cell interactions in Arabidopsis, encodes a putative lipid biosynthetic enzyme Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)		
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REFERENCE	Prittc,R.E., Vielle-Calzada,J.-P., Ploense,S.E., Grossniklaus,U. and Fiddlehead, a gene required to suppress epidermal cell interactions in Arabidopsis, encodes a putative lipid biosynthetic enzyme Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)		
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REFERENCE	Prittc,R.E., Vielle-Calzada,J.-P., Ploense,S.E., Grossniklaus,U. and Fiddlehead, a gene required to suppress epidermal cell interactions in Arabidopsis, encodes a putative lipid biosynthetic enzyme Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)		
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REFERENCE	Prittc,R.E., Vielle-Calzada,J.-P., Ploense,S.E., Grossniklaus,U. and Fiddlehead, a gene required to suppress epidermal cell interactions in Arabidopsis, encodes a putative lipid biosynthetic enzyme Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)		
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REFERENCE	Prittc,R.E., Vielle-Calzada,J.-P., Ploense,S.E., Grossniklaus,U. and Fiddlehead, a gene required to suppress epidermal cell interactions in Arabidopsis, encodes a putative lipid biosynthetic enzyme Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)		
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REFERENCE	Prittc,R.E., Vielle-Calzada,J.-P., Ploense,S.E., Grossniklaus,U. and Fiddlehead, a gene required to suppress epidermal cell interactions in Arabidopsis, encodes a putative lipid biosynthetic enzyme Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)		
REFERENCE	10655527		
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RESULT 7
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DEFINITION Arabidopsis thaliana fiddlehead protein (fdh) gene, fdh-3 allele,
complete cds.
ACCESSION AF214496
VERSION AF214496.1 GI:8177710
KEYWORDS
SOURCE
ORGANISM
2 of 2
Arabidopsis thaliana.
Arabidopsis thaliana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
Pruitt,R.E., Vielle-Calzada,J.P., Ploense,S.E., Grossniklaus,U. and
Lolle,S.J.
FIDDLEHEAD, a gene required to suppress epidermal cell interactions
in Arabidopsis, encodes a putative lipid biosynthetic enzyme
Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)
10655527
2 (bases 1 to 1425)
Pruitt,R.E., Vielle-Calzada,J.P., Ploense,S.E., Grossniklaus,U.
and Lolle,S.J.
Direct Submission
Submitted (13-DEC-1999) Molecular and Cellular Biology, Harvard
University, 16 Divinity Avenue, Cambridge, MA 02138, USA
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AUTHORS	1 (bases 1 to 1425) Pruitt, R.E., Vielle-Calzada, J.P., Ploense, S.E., Grossniklaus, U. and Lolle, S.J.		
TITLE	FIDDLEHEAD, a gene required to suppress epidermal cell interactions in Arabidopsis, encodes a putative lipid biosynthetic enzyme		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)		
MEDLINE	20122614		
PUBMED	10655527		
REFERENCE	2 (bases 1 to 1425) Pruitt, R.E., Vielle-Calzada, J.P., Ploense, S.E., Grossniklaus, U. and Lolle, S.J.		
AUTHORS	Direct Submission Submitted (13-DEC-1999) Molecular and Cellular Biology, Harvard University, 16 Divinity Avenue, Cambridge, MA 02138, USA		
TITLE	Location/Qualifiers		
JOURNAL	1. 1425		
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 1 (bases 1 to 1425)
 Pruitt,R.E., Vielle-Calzada,J.P., Ploense,S.E., Grossniklaus,U. and
 Lolle,S.J.
 FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 in Arabidopsis, encodes a putative lipid biosynthetic enzyme
 Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)
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 2 (bases 1 to 1425)
 Pruitt,R.E., Vielle-Calzada,J.P., Ploense,S.E., Grossniklaus,U.
 and Lolle,S.J.
 Direct Submission
 Submitted (13-DEC-1999) Molecular and Cellular Biology, Harvard
 University, 16 Divinity Avenue, Cambridge, MA 02138, USA
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 VERSION AF337910.1 GI:12597466
 KEYWORDS FLI-CDNA.
 SOURCE Arabidopsis thaliana.
 ORGANISM Arabidopsis thaliana.

REFERENCE
 AUTHORS Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
 Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
 Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
 Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
 Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
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 Davis,R.W., Ecker,J.R. and Theologis,A.
 Arabidopsis Full Length cDNA Clones

TITLE
 JOURNAL Arabidopsis Full Length cDNA Clones
 AUTHORORS
 REFERENCES
 2 (bases 1 to 1927)
 Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
 Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
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 Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
 Satou,M., Seki,M., Shimu,P., Southwick,A., Shinozaki,K.,
 Davis,R.W., Ecker,J.R. and Theologis,A.
 Direct Submissions

TITLE
 JOURNAL Arabidopsis Full Length cDNA Clones
 COMMENT
 Submitted (19-JAN-2001) Plant Gene Expression Center, 800 Buchanan
 Street, Albany, CA 94710, USA
 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RFLV cDNAs (RFLV cDNA: RIKEN
 Arabidopsis Full-Length cDNA).: Seki,M., Narusaka,M., Ishida,J.,
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
 Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the
 sequencing and annotation of the RFLV cDNAs: Yamada,K., Liu,S.X.,
 Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D.,
 Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Chen,H.,

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PT	for identifying herbicides, and of its nucleic acid for identifying
PT	specific modulators .
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PS	Claim 9; Page 13-17; 22pp; German.
CC	The invention relates to use of a polypeptide with very long chain fatty
CC	acid elongase (VLCFAE) activity for identifying herbicides. The protein
CC	and the nucleic acid that encodes it, are used to identify compounds,
CC	including herbicides and plant-growth regulators, that alter activity or
CC	expression of the protein. The nucleic acid is also used to produce
CC	transgenic plants with altered activity or expression of the protein and
CC	for recombinant preparation of the protein. The invention relates
CC	especially to the fiddlehead (<i>fhd</i>) protein (GenBank Accession Number
CC	CAH09311) and encoding DNA sequence (GenBank Accession Number AJ010713)
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RESULT 3
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
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XX 30-NOV-1993; 93US-0160602.
XX (CALJ) CALGENE INC.
XX Lardizabal KD, Lassner MW, Metz JG;
XX WPI: 1995-215267/28.
XX P-PSDB; AAR77166.
XX Production of very long chain fatty acid(s) in plant(s) - to produce
XX drought and stress resistant transgenic plant(s)
XX
XX Claim 5; Figure 5; 149pp; English.
XX
XX Arabidopsis locus 39823 [sometimes called 398293] in Genbank
XX accession Z26005 is homologous to joboba beta-ketoadyl CoA
XX synthase DNA sequence. Two primers were synthesised - 090226
XX and 090227. 090226 corresp. to the peptide NITR16, which is Aas
XX 389-394 of the joboba beta-ketoadyl-CoA synthase, and 090227
XX corresp. to the peptide SNCRG, which is Aas 525-532 of the
XX joboba beta-ketoadyl-CoA synthase. These primers encode the
XX sense and antisense strands of the respective peptides. The primers
XX amplify an approx. 430 bp. DNA fragment from both the joboba
XX beta-ketoadyl-CoA synthase cDNA and the Arabidopsis 398293
XX sequence. Using the degenerate oligos, Arabidopsis green siliques,
XX HBAR, and LEAR RNA were subjected to RT-PCR. Prominent bands of the
XX expected size were amplified from all 3 RNAs. One clone obtd. from
XX the restion PCR reaction, and 2 clones from the 212/86 reaction,
XX which appear to be from two classes of cDNA clones, designated CE15
XX and CE20. The 212/86 CE15 clone encoded the entire CE protein
XX (090210/R77166). CE15 is expressed at high levels in leaves and at
XX a much lower level in developing seeds. The protein sequences of
XX CE15 and CE20 are almost identical. CE20 is highly expressed in
XX developing seeds and at very low levels in leaves.
XX
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XX
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XX Best Local Similarity 81.3%; Pred. No. 7.4e-171;
XX Matches 1188; Conservative 0; Mismatches 183; Indels 91; Gaps 6;
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RESULT 7
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DT 18-OCT-2000 (first entry)
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KV Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
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PF 25-FEB-2000; 2000EP-0301439.
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PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
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PR 19-JUL-1999; 99US-0144331.
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PR 26-JUL-1999; 99US-0145276.
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PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
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Db 1199 AGCCATACATCCAGATTTCAGATTGGCAGCGAAGCACTTCATCCATCGAGAGGCA 1258
 QY 2146 AAGTAGCTCTGAGAGCTTCAAAAGAAATCTAGGCTTGAGTGAAGAAATATGAGGCTT 2205
 Db 1259 AAGCAGTGTGATGATGCTCGAGACGAACTTGAGTTGACGGCATGGCACTTGAACCT 1318
 QY 2206 CTAGAGTACACTTCAGAGTTTGGAAACACTTTCAGCAGTGAATCTGGTATGAGTTGG 2265
 Db 1319 CGAGATGACACTGTATGAGTTTGGGAACACATCGAGTGCATATATGATGATGAGTTGG 1378
 QY 2266 CTACATGAGAGCCCAAGAAATGTTCTCGTAGGCGGATGAGTTGGCAGATCGCTTTGG 2325
 Db 1379 CATAGCTGAAACCAAGGAGAGATCCGTAAGGTGATCGAATCTTGATGATGATTTGG 1438
 QY 2326 GTTCGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2385
 Db 1439 GTTCAGTTTCAAGTGTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1498
 QY 2386 CCAGAGCAATCTTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2445
 Db 1499 GAGAGAGAAATCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1558
 QY 2446 TTCTCTTAAT 2457
 Db 1559 CACCTATCGCTT 1570

RESULT 9

AA090208 standard; cDNA, 1783 BP.

AA090208;

04-DEC-1995 (first entry)

Jojoba fatty acyl-CoA cytoplasmic protein cDNA in pCGN7614.

Very long chain fatty acid; fatty acyl-CoA; ss.

Jojoba.

Key Location/Qualifiers
 CDS 10..1575
 /*tag= a

M09515387-A.

08-JUN-1995.

30-NOV-1994; 94WO-US13686.

23-JUN-1994; 94US-0265047.

30-NOV-1993; 93US-0160602.

(CALJ) CALGENE INC.

Lardizabal KD, Lassner MW, Metz JG;

MPI; 1995-215267/28.

P-PSDB; AAR77165.

Production of very long chain fatty acid(s) in plant(s) - to produce drought and stress resistant transgenic plant(s)

Example; Fig 3; 14pp; English.

RNA is isolated from Jojoba embryos and used to construct a cDNA library. Synthetic oligos are synthesised which corresp. to the AA sequences of selected peptide fragments and segments of DNA are produced. The DNA fragments obtd. by PCR are labeled and used as a probe to screen clones from the cDNA libraries. An approx. 1500 nt. Jojoba cDNA clone is obtd. in this manner. Comparison to the peptide fragments in AAR77175-R77182 reveals the presence of

CC each of these peptides in the translated sequence, with the exception of S01129. The mRNA is approx. 2kb. Preliminary DNA sequence of a Jojoba gene is presented in AA090107/R77164. Further DNA sequence analysis of additional clones indicates that there are at least 2 classes of cDNAs encoding this Jojoba protein. The cDNA plasmid contg. the entire coding region in pCGN1703 is constructed to contain a SalI site approx. 8 nts 5' to the ATG start codon and is designated pCGN7614. The complete DNA sequence of pCGN7614 is given in AA090208/R77165. The major difference between the two classes of cDNAs is the presence (AA090207) or absence (AA090208) of the 6 nt coding sequence for AAs 23 and 24 of AAR77164.

Sequence 1783 BP; 450 A; 446 C; 432 G; 455 T; 0 other;

Query Match 10.7%; Score 296.8; DB 16; Length 1783;

Best Local Similarity 55.2%; Pred. No. 2.3e-48; Matches 735; Conservative 0; Mismatches 447; Indels 150; Gaps 2;

QY 1126 AAGAGAGTTCATAGAACTAGAGAGAAATCAGGAGTTGACGAGAGACCTCGGTT 1185
 Db 389 ACGAGATGTTCAATGAGACCGGACCTCCCGGGCGGGTCTTCTAAGAGAAATATGAGT 448
 QY 1186 TCAAGAGAGAGATCTTACAGGCTCAGGATAGGCGAGAGACATACGTCCTCAAGATCCA 1245
 Db 449 TTCAGAGAGAGATCTTGGAGAGGCGGATATGGCGGAGAACTTACGTCCTCCGAATCG 508
 QY 1246 TCTCTTCATCAGAAACATATACAGATGAGAGAGAGTGTGAAGAGCTCTACAGTGA 1305
 Db 509 TCACATAGAGTGGCGCCGACCGAGCATAGCAGCAGCCGAGGCGGAGAGAGATGA 568
 QY 1306 TCTTGGAGACTAGACGAACTCTTCGAGAGACAGCTGTAAACCTTAAGAGCTTGGTG 1365
 Db 569 TGTACGGGGCGATGACGAGGATGTTGAGAGAAACGGGGGTGAAGCCGAGATAGGAA 628
 QY 1366 TCTTGTGTGATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1425
 Db 629 TACTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 688
 QY 1426 ACCATTACAGAGATGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1485
 Db 689 ACCATTACAGAGATGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 748
 QY 1486 CTGGAATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1545
 Db 749 CTGGGCTCATTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 808
 QY 1546 CTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1605
 Db 809 TGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 868
 QY 1606 TGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1665
 Db 869 TGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 928
 QY 1666 GTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1725
 Db 929 GCGGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 988
 QY 1726 CTGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1785
 Db 989 CTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 996
 QY 1786 ACCGAGCTAGTAACTAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1845
 Db 997 -----AAGTCTATAGATGGCTCTTACACAGAGAAATGAAA 1033
 QY 1846 AAGATTCAGAGGTTGAAGATAGTATGAGACTTAATGAGAGAGTGAAGTGAAGTCTCA 1905
 Db 1034 ATAAAGAGT 1093
 QY 1906 AAGCAAACTACTACTAGT 1965
 Db 1094 AGGCCAACTACAGACCTTGT 1153

PR 08-JUL-1999; 99US-0142803.
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PR 29-OCT-1999; 99US-0162142.

Query Match 10.5%; Score 292.2; DB 21; Length 1824;
Best Local Similarity 55.8%; Pred. No. 1,8e-47;
Matches 740; Conservative 0; Mismatches 443; Indels 142; Gaps 4;

QY 1128 GAAGAGTTATGAGATACGAGAAATATCAGGAACTTCGACAGAGACTCGGTTT-1186
DB 519 GAACACTTATGACAGATCTCAACGTGTAGCATTTACACAGACAACTTACTTTC
QY 1187 CAGAAGAGATCTTACAGCCTCAGCAGATAGCGAGACATACCTCCAGATTCAT-1246
DB 579 CAACAAAGATCCTCGAAGAAATCCGCTAGTGAAGAACTTACTTCCCTGAACCTCT-638
QY 1247 CTCCTATATGAGAAACATTAACACGATGAAGAGTCTGAAGAACCTTACATGAT-1306
DB 639 TCTTCGTTCCTCCATATCTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG-698
QY 1307 CTTTGAGCAGTATGAGACATCTTCGAGAGAGACAGTAAACCTAAAGACCTTGCTG-1366
DB 699 GTTCGAGCTATGAGACCGCGTCTTGAAGAGACCGGTGGAACCTTAAGATTTGGAA-758
QY 1367 CCTGTGTGTTAACTAGATTTTCAACCCGACACCGTGTGTGCGCAATGGTGAATA-1426
DB 759 CCTGTGTGTTAACTAGATTTTCAACCCGACACCGTGTGTGCGCAATGGTGAATA-818
QY 1427 CCATTCAGATGAGAGGAGACATTAATGTTTCAACCTTGGAGGATGGATGTTGCGC-1486
DB 819 TAAGTATTAAGCTTAAAGGAGCAATTTTGAAGTATTAATCTTGTGGAATGGATGATG-878
QY 1487 TGAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG-1546
DB 879 TGCCCTATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG-938
QY 1547 TGTGTGTGAGTACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG-1606
DB 939 ACTAGTGTGAGACAGACAGAGACATTAACCTTAACCTGATGATGATGATGATGATGATGAT-998

Db 816 TGTTCAGTGAACATTACTCAGATTGTAATTTGGTAACAGAAATCATGTTGAT 875
Qy 1613 ACCTAATTTGTTCTTAGAGATGGTGTCTCCGTTATGCTCTTAACCGTGTGTGA 1672
Db 876 ACCGAACCTGCTGTGTTGAGTGGTGGCTCTCGGTTTTCATCGAACAAGTCGAGGGA 935
Qy 1673 CTTTCGCCATGTCATACCGTCTCAGACATTTGCCAAGCATTAAGGCTCTGACGA 1732
Db 936 CAAGAGACGCTCTAATACAGGCTTTACATGTAGTCAGACCTACCGTGGACAGATGA 995
Qy 1733 CCGTACCTCAGGTTTCATTCATTTGGTAATTCGTTTACAAATCTTCGACCGACC 1792
Db 996 ----- 995
Qy 1793 TAGTAACTAATTTTGTGCTTTTGAAGAGTGTCTACCGAAGAAAGATGAACAGATT 1852
Db 996 -----TAAAGCTTCCGTTGTGTTTATCAAGACAGATATACAGGAG 1040
Qy 1853 CAAGGGTTGAGATAGATAGAGACTTAATGSAAGTGGAGTGAAGCTCTCAAGCAAA 1912
Db 1041 AACCGGGGTTTCTTCGAAAGATCTAATGGCATTCAGGGGAACCTCAAAACCAA 1100
Qy 1913 CATCACTACCTTAGTCTCTTGTCTTACCTTCTCCGACAGCTTCTCTTCTTGTGTC 1972
Db 1101 TATCACTAATTTGGTCTCTTGTCTTACCGATAGAGACAGATTCCTCTT----- 1155
Qy 1973 TTGTGCTCCGCCGACATTTCTACCTCTGCGCAAAAGCTCCACAACCACTTCTCTAC 2032
Db 1156 ----- 1155
Qy 2033 TTCCGCCACCGCAAAACCAATGAAATCAAGTCTCTCTCCGATCTGTCCAAGCATTA 2092
Db 1156 -----ATGACTCTAGTTGTGAGAAAGCTCTTAAACGTAAGTGAACCGTA 1202
Qy 2093 CATCCGGACTACAGCTCGCTTCGAGCAATTTTCTTCCACGCGCAAGCAAGTAGT 2152
Db 1203 TATCCGGATTTCAAACTGCTTCGAGCATTTCTGTATCCATGCTGGTGAAGAGCTGT 1262
Qy 2153 GCTTGAAGAGCTTCAAAAGATCTAGCTTGAAGTGAAGAAATATGAGAGCTTCTAGAT 2212
Db 1263 GATCGATGAGTGAAGAAAGATCTGACGCTTTCACAGTCAATGATGAGGCTTGAAGAT 1322
Qy 2213 GACACTTTCAGGTTTGAAGAACTCTAGCAGTGAATCTGTATGAGTGTGCTTACAT 2272
Db 1323 GACTCTTCACTGATTTGGTAACATCTTCGACCTCATTTGGTAAGATTTGGCTTACAT 1382
Qy 2273 GGAGGCCAAGAAAGTGTCTGAGAGCGATAGGGTTTGGCAGATGCTTTCGTTCTGG 2332
Db 1383 TGAAGCGAAGGAGATGCGAAGAGTAAATCTGTTTGGCAAAATCGCGTTGGAAGTGG 1442
Qy 2333 TTTTAACTGTAACAGTGTGTGTGGAAGCAATGAGGAAGTGAAGCAACGAGGA 2392
Db 1443 ATTAAATGTAATGAGCGCATTTGGGAAGCATTAAGGCAAGT---GAACCTTCGAACAA 1499
Qy 2393 CAATCTGGTGGTATGATCAACCGTTACCTGTGCTCT 2434
Db 1500 CAGTCTCTGGGAAGATTGTATTGACAAGTATCCGTTACTTT 1541

RESULT 13

AAC42778
ID AAC42778 standard; DNA; 1464 BP.

AC AAC42778;

DF 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36814.

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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PR 28-APR-1999; 99US-0130891.
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PR 05-MAY-1999; 99US-0132484.
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PR 11-MAY-1999; 99US-0132863.
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PR 10-SEP-1999; 99US-0153070.
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PR 21-OCT-1999; 99US-0160776.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 10.1%; Score 281.6; DB 21; Length 1464;
Best Local Similarity 55.7%; Pred. No. 2e-45;
Matches 713; Conservative 0; Mismatches 414; Indels 153; Gaps 3;

OY 1162 AGTTGAGAGAGACACTCGTTTCAGAGAGATCTTACAAACCTCAGGCATAGCGC 1221
DB 335 ATTTCAGGAAACCTCTCTGTGATTCAGAGAGATCTTGTTCGGTG 394
OY 1222 ACGAGACATACGTCACAGATCATCTCTCATCAGAAACATACAGATGAAGAAG 1281
DB 395 AAGAGACTTATTACCGGATTCATCTATCCCTCCGGTCTTACTATAGCTGACG 454
OY 1282 GTGCTGAAGAACCTCTACAGTATCTTGGACACTAGAGACATCTTCGAGAAGAC 1341
DB 455 CCGCTGAAGAACCGGAGCAGTAATCTCGGTCACCTGCACATCTTTTCGAGATACA 514
OY 1342 GTGTAAACCTTAAGACGTGGTCTTCTTGCTTGCTTAAGCTATGACATTTTCAACCCGACAC 1401
DB 515 AATCAATCCTTAGAGAGATGGTGTCTTGTGTAATGTAGTTGTTAAACCTTACGC 574
OY 1402 CGTCGTCGCCCATGGATGATTAACCATTAACAAGATGAGAGAACATTAAGTTACA 1461
DB 575 CTTCCTTATCCGCCCATGATGTTAACAAGTAAACCTTAGAGAACATTAAGACTTTA 634
OY 1462 ACCTTGAGAGATGGATGCTCGCTGGAATCATAGTATGATCTCTGCTGACATGC 1521
DB 635 ACCTTGAGAGATGGAGTACTGCTGGTATATCGCGTAGATAGTACTAGTATATGT 694
OY 1522 TTCAGCTAACCTTAATAGTTATGCTGTGTGTGTAGTACAGTACAGTATGTTGGTATAT 1581

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Db 695 TACAATGCAATGAGAACACTTTGCTTGTGTTAGTACGTGAGAACATCACTCAGAAAT 754
Oy 1582 GGTACGTGGGAAGTACACATGATGTTATACCTAATTTCTTTAGAGAGGTTGTT 1641
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Db 755 GGTATTTTGGTAAAGAACAAAGTGTGATCCCTAATTTGCTTTAAGTTGGGTT 814
Oy 1642 CTGGCGTTATGCTCTGATGCGTTCGCTGCTTTCGCTTCTAGTCCGCTCGAGC 1701
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Db 815 CCGCGTTTCTGCTTTGACAAAGCCCTTGGATCGAAAGATCGAATTAAGCTTGTTC 874
Oy 1702 ACATTTCCGACATCATAGGCTGCTGACGACCGTACGTTTCTAGTTTCTTATTTGGT 1761
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Db 875 ATACGCTGACGACATCAATAGATCTGATGAGAACGACATTCATTT----- 919
Oy 1762 ATTAATGCTTTTACAATCTCTTGACCGACCTAGTAACTAATTTTGTGTTTGAAGA 1821
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Db 920 ----- 919
Oy 1822 GGTGTACCGAGAGAGATGAAACAAGATTCAGGGGTTGAAGTAAAGTACGACTTAA 1881
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Db 920 GGTGTATACAGAACAAAGATGATGTTGAAACCGGACTTCTTGTCTTAAAGATCTTA 979
Oy 1882 TGGAGTTGGAGTGAAGCTCTCAAGACAAACATCACTACCTTAGTCTCTTGTCTTAC 1941
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Db 980 TGGCTATAGCTGGAGAAAGCTTAAAGACAAATATCACTCTTGGGCTCTGTGTTCTTC 1039
Oy 1942 CTTCCTCGAGAGCTTCTCTTCTTGTGCTTGTGCTCGCGGACATTTCTACCTGCTG 2001
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Db 1040 CTATAGAGGACGAGATTTGTTCTTGTGCGACTTTGT----- 1076
Oy 2002 CCAAAAGCTCACAAACACTTCTCTCTACTTCGCGCACCGCAAAACCAATGGAATTA 2061
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Db 1077 -----TGCATAA 1084
Oy 2062 AGTCTCTCTCTCCGATCTGTCGAAGCCATCCGAGCTACAGACTCGGCTTCGAGC 2121
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Db 1085 GATTTCTCATGTACAAGAAAGAACCCCTTACATCCGATTCAGCTTGTCTTGTGATTC 1144
Oy 2122 ATTTTGTCTTCACCGCGGCAACAAAGTATGCTTGAAGAGCTTCAAAAGATCTTAGC 2181
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Db 1145 ATTTCTGATTTACCGGGAGGTAGAGCCGTATGTATGATGATGATGAGAGATTTAAAGC 1204
Oy 2182 TGAAGTGAAGATATGAGAGCTCTAGATGACACTTCAAGGTTTGAACACTTCTA 2241
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Db 1205 TTTCTCCAAAACATGTTGAGGCGCTCAAGATGACTTTGATGATTTGAAACACTTCT 1264
Oy 2242 GCAGTGAATCTGTATGATGCTTACATGAGGCGCAAGAAAGTCTCTAGAGCG 2301
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Db 1265 CTAGCTCTATATGATGATGATGCTTACACGAAAGCTAAAGAAATGAGAAAGGAA 1324
Oy 2302 ATAGGTTTGGAGATCCGCTTCGTTGCTGTTTAAAGTGAACGTTGCTGTCGAAG 2361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1325 ACAGAGTTTGGAGATGCTTTTGGAGCGGTTTAAAGTAAACGCGGTTTGGGTGG 1384
Oy 2362 CAATGAGAGGTGAAGAAGCAACACAGAACATCTTGGGTGATGATCAATCACTT 2421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1385 CTCTTCGCAATGT---CGAGCCCTCGGTTAAACAATCCTTGGGAACTTGCATCAATGAT 1441
Oy 2422 ACCCTGCTCTCTTAATTT 2441
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1442 ATCCGCTTAAAGATGATCTT 1461
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RESULT 14

AAf62693 standard; DNA; 2509 BP.

AAf62693:

08-MAY-2001 (first entry)

Arabidopsis KCS2 genomic DNA.

XX

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KW Long chain fatty acid condensing enzyme: KCS2;
KM beta-ketoacyl-coenzyme A synthase 2; cosuppression; antisense;
KW screening; ds.
OS Arabidopsis sp.
PN W0200107586-A2.
XX
XX
XX 21-JUL-2000; 2000WO-CA00860.
XX 01-FEB-2001.
XX 22-JUL-1999; 99US-0145013.
XX
XX (UYBR-) UNITV BRITISH COLUMBIA.
XX
XX Kunst L, Clemens S;
XX
XX WPI: 2001-168548/17.
XX
XX Novel nucleic acid sequence encoding plant long chain fatty acid (LCFA)
XX condensing enzyme (fatty acid elongase) useful for producing transgenic
XX plants having altered fatty acid content in the tissues
XX
XX Example 1; Fig 1; 32pp; English.
XX
XX The present invention relates to a plant long chain fatty acid
XX condensing enzyme, KCS2 (beta-ketoacyl-coenzyme A synthase 2).
XX The invention is useful in cosuppression or antisense inhibition,
XX as a plant breeding tool, as molecular markers to aid in plant
XX breeding programs and in screening
XX
XX Sequence 2509 BP; 748 A; 478 C; 497 G; 786 T; 0 other;
XX
Query Match 10.1%; Score 281.6; DB 22; Length 2509;
Best Local Similarity 55.7%; Pred. No. 2.2e-45;
Matches 713; Conservative 0; Mismatches 414; Indels 153; Gaps 3;
Oy 1162 AGTTCAGCAAGAGACACTCGCTTTCAGAAAGATCTTACAGCTCAGCATGAGCG 1221
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Db 1380 ATTTACAGCAAACTTCTTGAAGTTCAGAGAAATCTTGATTCGCTGTGCTGCGTG 1439
Oy 1222 ACAGACATACGCTCCCAAGATCACTCTTCAAGAAACATTAACAGATGAAGAG 1281
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Db 1440 AAGAGCTTATTTACCGGATTTCTATCACTATCCCTCGGCTCTACTATGCTGCG 1499
Oy 1282 GTCTGAGAAAGCCCTCTACAGTATCTTGGAGCACTAGACGAACCTTCGAGAAACAC 1341
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Db 1500 CCGGTGAAGAAAGCGAGCAAGTATCTTGGGCACTCGACATCTTTTCGAAATACAA 1559
Oy 1342 GTGTAAACCTTAAGACGTTGCTGCTTGTGTTAACTGATGATTTCAACCCGACAC 1401
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Db 1560 AATCAATCTTAGGAGATTTGCTTGTGTTGATGATTTGTTTAAACCTTACGC 1619
Oy 1402 CGTCTGTTCCCAATGATGATTAACATTACAGATGAGAGGAACATACTTATTAGA 1461
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Db 1620 CTCTTTATCCCGCATGATTTGTTAAACAATTAAGTTAGAGAAACATTAAGAGCTTTA 1679
Oy 1462 ACCTTGAGAGATGGAGTTCGCTGGAATCATAGCTATGATCTTGTGCTGACATGC 1521
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Db 1680 ACCTTGAGAGAAATGGATGTAGTGTGTTATCCGCTAGATCTAGCTAGATGATATG 1739
Oy 1522 TTCACTTAACCTTAATAGTTATGCTGTTGTGTGATGCTAGATGCTTGGTATAAT 1581
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Db 1740 TACAATAATCATAGGAACACTTTTGTCTTGTGTTAGTACTGAGAACATCACTCAATAAT 1799
Oy 1582 GGTACGTGGAAGTGAACATGATGATGATTAACCTTATGTTCTTCTTATGATGGGTTGTT 1641
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Db 1800 GGTATTTTGTAAACAAGAAAGCAATGTATCCCTAATTTGCTTTTAAAGTTGGGTT 1859
Oy 1642 CTGCGTTATGCTCTTAACCGTCTGCTGATTTTCCCATGCTAAGTACCTCTGAGC 1701
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Db 1860 CCGGCTTCTGCTTTCGACAAAGCCTTTGGATCGAAAGATCAAGTAAAGCTTGTTC 1919
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PR 08-JUL-1999; 99US-0142803.
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PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 06-OCT-1999; 99US-0157865.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 10.0%; Score 278; DB 21; Length 1587;
Best Local Similarity 54.9%; Pred. No. 1e-44;
Matches 700; Conservative 0; Mismatches 430; Indels 144; Gaps 2;

QY 1122 ACAAGAAGAGTTCTAGACACTAGCAGAAATCAGAGGAGTTCGACGAGACATC 1181
DB 364 ACAAGAGAAACGTTACATGACCGGCTCAGCCGTGCTGATCTTCCACAGAACACCTC 423
QY 1182 GATTTCAGAGAGAGATCTTCAAGCCTCAGCATAGCCGACGACGACATACGTCACAGA 1241
DB 424 GCTTCCACAAAGAAATCCGACGATCGGCTTGAGACAAAGACTTACTTCCCGAG 483
QY 1242 TCCATCTCTTCATCAGAAACATACACAGCATGAAAGAGGTGTCAGACAGCCTTACA 1301
DB 484 GCTCTCTTACGTGTCGCCGCTTAATCTTGTATGCTGAAACAGGAAGAGCCGAGACG 543
QY 1302 GTGATCTTGGAGCAGTACGAGCAACTCTCGAGAAAGACAGTAAACCTAAAGAGCT 1361
DB 544 GTTATGTTTGGAGCTATAGCGCAGTCTTGAGAAAAACCGAGTGAATCTTAAGATAT 603
QY 1362 GGTGCTCTTGTTGTTACTCTAGTATTCACACCGACACCGTGTGTCGCAATGTG 1421
DB 604 GGGATCTTGTCTGTAATGTCTTACCTTTAAATCCGACGCTTCGTTATGCGTATGATC 663
QY 1422 ATAAACCATTACAAGATGAGAGGAGAAACATTAAGTTACACCTTGAGAGGATGGATGT 1481
DB 664 GTAAATTAATATATAGCTCAGGAGAAACGTTTGTAGCTATTAACCTGTGTAATGGAT 723
QY 1482 TCGGCTGGAATCATAGTATTTGATCTTGTGTCGAGCATGTTAGCTTAACCTAATAGT 1541
DB 724 AGTGTGCTTATCTTCCATTAATCTGCTAAACAGCTTTTATAGTTCAACCAATATCA 783
QY 1542 TATGCTGTGTTGTGAGTACTGATGATGTGGTATTAATGTACGTGAGACGACGAAG 1601
DB 784 TATGCACTGATAGTACGACAGAGAAACATTAACCTTAACCTGATATTTAGCAACGACGA 843

QY	1117	AGGTGACAAAGAAAGAGGCTTCATGAACTAGCAGCAAAATCAGGAGAACTTCACGCAAGAGA	1176
Db	407	AGGTGACAAAGAAAGAGGCTTCATGAACTAGCAGCAAAATCAGGAGAACTTCACGCAAGAGA	466
QY	1177	CACTCGGTTTCAAGAAAGAGGATCTTACAAGCCTCAGGCATAGGCGACGAGACATACGTC	1236
Db	467	CACTCGGTTTCAAGAAAGAGGATCTTACAAGCCTCAGGCATAGGCGACGAGACATACGTC	526
QY	1237	CAGATGCCATCTCTTATCAGAAAAACATAACAACGATGCAAAAGTGCTGTAAGAAAGCT	1296
Db	527	CAGATGCCATCTCTTATCAGAAAAACATAACAACGATGCAAAAGTGCTGTAAGAAAGCT	586
QY	1297	CTACAGTGATCTTTGAGAGCACTAGACGAACCTTTCAGAGAAGACACGTTGTAACCTTAAG	1356
Db	587	CTACAGTGATCTTTGAGAGCACTAGACGAACCTTTCAGAGAAGACACGTTGTAACCTTAAG	646
QY	1357	ACGTTGGTGCTCTGGTGTTAACTGTAGATTTTCAACCCGACACCGTGCTGTCGGGA	1416
Db	647	ACGTTGGTGCTCTGGTGTTAACTGTAGATTTTCAACCCGACACCGTGCTGTCGGGA	706
QY	1417	TGGTGTATTAACCATTAACAAGATGAGAGGGAGACATCTTAGTTACAACCTTGAGGGATGG	1476
Db	707	TGGTGTATTAACCATTAACAAGATGAGAGGGAGACATCTTAGTTACAACCTTGAGGGATGG	766
QY	1477	GAGTTCCGCTGGAATCATAGCATTTGATCTTGCTCGTACATGCTCAGTCTAACCTTA	1536


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QY 1546 CTGTTGTTGAGTACTGAGATGTTGGGTATATATGTAAGTGGAGAGTACAGTCAA 1605
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Db 809 TGTATGATGAGCAGACAGAAACATACCTTATTTGTAAGTGGAGAGTACAGTCAA 868
QY 1606 TGGTATATACCTAATTTCTTTCTTTAGAGTGGTGTCTGCGCTTATGCTCTACCGTTC 1665
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 869 TGGTATATACCAACTGCTATTTGCGATGGTGGCGCTGCATCATCTCTTCAACCGGT 928
QY 1666 GTGCGTACTTTGGCCATGTAAGTACCGCTGAGCAGCATTTGCCAATCATTAAGGCTG 1725
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 929 GCGGTGATGTCGCCGATCCAGTACCAACTCTCTTCAACAGTACCCAGCCAGGCGG 988
QY 1726 CTGACGACGCTGAGCTTCAGGTTTCATTTTGTATTAATTCGTTTACATCTCTTG 1785
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 989 CTGACGAC----- 996
QY 1786 ACCGACCTGATACATAATTTGTGTGTTTATGAGTGTACAGAGTGAAGATGAAC 1845
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 997 -----AAGTCTATGATGCGCTTACAAACAGAGATGA 1033
QY 1846 AAGGATTCAGGGGTTGAAGATAGTAGAGACTTAATGGAAGTGAAGTGAAGCTCTCA 1905
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1034 ATAAACAGGTAGGTGTGCTTATCCAGAGATCTGATGCGAGTTGCCGGAAGCCCTTA 1093
QY 1906 AGACAAACATCACTACCTTACCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 1965
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1094 AGGCCAATCATCAGACACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTCT 1153
QY 1966 TTGCTGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2025
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1154 TTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
QY 2026 TCTCTACTTCCGCGACCGGAAAAACCAATGGAATCAAGTCTCTCTCTGATCTGCA 2085
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1198 -----A 1198
QY 2086 ACCATACATCCCGGACCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2145
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1199 AGCCATACATCCCGGACCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1258
QY 2146 AAGTATGCTTGAAGAGCTTCAAAAGATCTAGGCTTGAAGAGATATGAGAGCTT 2205
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1259 AAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1318
QY 2206 CTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2265
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1319 CGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1378
QY 2266 CTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2325
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1379 CATACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1438
QY 2326 GTTCTGCTTGAAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 2385
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1439 GTTCTGCTTGAAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1498
QY 2386 CCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2445
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1499 GAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1558
QY 2446 TTCTCTTAATTT 2457
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Db 1559 CACCTATGCTT 1570

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RESULT 3

US-08-265-047-3

; Sequence 3, Application us/08265047

; Patent No. 5679881

; GENERAL INFORMATION:

; APPLICANT: Metz, James G.

; APPLICANT: Iardizabal, Kathryn D.

```

? APPLICANT: Lassner, Michael
? TITLE OF INVENTION: Nucleic Acid Sequences Encoding a Plant Cytoplasmic Protein
? NUMBER OF SEQUENCES: 16
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Calgene, Inc.
? STREET: 1920 Fifth Street
? CITY: Davis
? STATE: CA
? COUNTRY: USA
? ZIP: 95616
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
? COMPUTER: Apple Macintosh
? OPERATING SYSTEM: Macintosh 7.0
? SOFTWARE: Microsoft Word 5.1a
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/265,047
? FILING DATE: 23-JUN-94
? CLASSIFICATION: 435
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: 08/160,602
? FILING DATE: 30-NOV-93
? CLASSIFICATION: 435
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: 07/796,256
? FILING DATE: 20-NOV-91
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: 07/933,411
? FILING DATE: 21-AUG-92
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: 08/066,299
? FILING DATE: 20-MAY-93
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: PCT/US92/09863
? FILING DATE: 13-NOV-92
? ATTORNEY/AGENT INFORMATION:
? NAME: Elizabeth Lassen
? REGISTRATION NUMBER: 31,845
? NAME: Donna E. Scherer
? REGISTRATION NUMBER: 34,719
? NAME: Carl J. Schwedler
? REGISTRATION NUMBER: 36,924
? REFERENCE/DOCKET NUMBER: CGNE 101-1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (916) 753-6313
? TELEFAX: (916) 753-1510
? INFORMATION FOR SEQ ID NO: 3 :
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1783 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? US-08-265-047-3
?
? Query Match 10.7%; Score 296.8; DB 1; Length 1783;
? Best Local Similarity 55.28; Pred. No. 2.1e-56;
? Matches 735; Conservative 0; Mismatches 447; Indels 150; Gaps 2;

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Db 569 TGTACGGGGGCGATGACGAGGTGTGGAGAACGGGGGTGAAGCCGAGATAGGAA 628
QY 1366 TCCCTGTGTAACTAGATATTTTCAACCGACACCGTGTGTCGCAATGAGATAA 1425
Db 629 TACGTGTGTAACTGACGCTTGTTAACCAAGCCGCTGTCATCATGATAGTA 688
QY 1426 ACCATTACAGATAGAGGAGAACATCTTACTTACAACTTGGAGGAGTGGATGTCGG 1485
Db 689 ACCATTACAGATAGAGGAGTAACTTACTTAACTTGGAGGAGTGGATGTCAGTG 748
QY 1486 CTGAATCATAGTATGTATGCTGTGTCGATGCTTCACTTCAACCTTAATAGTTAG 1545
Db 749 CTGGGCTCATTTCAATGATATTTGCAAGAGACCTCTTACAGGTTTACCGTAAACATATG 808
QY 1546 CTGTGTGTGTAGTACTGAGATGTTGGGTATTAATGTGTAGTGGAGATGACAAGTCAA 1605
Db 809 TGTATAGATAGACAGAAACATGACCCCTTAATGTGTACTGGGCAATGACCGCTTCA 868
QY 1606 TGTATTAATCTAATTTGTTCTTATAGATGGTGTGTCGCGTATGCTCTTAAACGTC 1665
Db 869 TGTATTAATCTAATTTGTTCTTATAGATGGTGTGTCGCGTATGCTCTTAAACGCT 928
QY 1666 GTGTGATCTTTCGATGCTAGTACGCTGTCGAGACATTTGCGAATGATAGGCTG 1725
Db 929 GGGGTGATCGTCCGATCCAGTACCAACTCTTCAACAGATGCGACCAACAGGCG 988
QY 1726 CTGACGACCGTGTAGCTGAGTTTCATTTGTTATTAATGCTTTTACAACTCTTG 1785
Db 989 CTGACGAC----- 996
QY 1786 ACCGACTAGTAACTATTTGTTGTTTATAGAGTGTGTACCGAGAGATGTAAC 1845
Db 997 -----AAGTCCCTTACATGCTCTTACACAAAGATGAA 1033
QY 1846 AAGATTCAAGGGGTGAAGATAGTAGAGACTTAATGAGAGTGGAGAGTGAAGCTTCA 1905
Db 1034 ATTAACAAGTAGTGTGTGCTTATTCAGAGATGATGAGCAGTGGCCGTAAAGCCCTAA 1093
QY 1906 AGACAAACATCACTTACCTTGTGCTTGTCTTCTTCTTCCGAGAGCTTCTTCT 1965
Db 1094 AGGCAACATCAAGCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1153
QY 1966 TGTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2025
Db 1154 TGTGCACTTATAGTGAAGTGTGCTTCAAGATGACCAAGCTG----- 1197
QY 2026 TGTCTACTTCCGACCGCAAAACCAATGATCAAGTCTTCCATCGATGTCGA 2085
Db 1198 -----A 1198
QY 2086 AGCCATATACCCGAGTACAGCTCGCTTCAAGATTTTGTCTTCCACGCGCAAGCA 2145
Db 1199 AGCCATATACCCGAGTACAGCTTGTGAGAGCAAGCACTTGTGATTCATGCAAGAGCA 1258
QY 2146 AAGTAGTCTTGAAGAGCTTCAAAAGATCTAGCTTGAAGAGAGATATGAGGCTT 2205
Db 1259 AAGTAGTCTTGAAGAGCTTCAAAAGATCTAGCTTGAAGAGAGATATGAGGCTT 1318
QY 2206 CTAGATGACACTTCAAGGTTTGAAGCAACTTACAGAGTGAATCGATGATGTTG 2265
Db 1319 CGAGATGACACTTATATGTTTGGAGACATGATGATGATGATGATGATGATG 1378
QY 2266 CTATACATGAGAGCAAGAAAGTGTGTAGAGGCAATGAGGTTTGGCAGATCTTTCG 2325
Db 1379 CATACGCTGAGAGCAAGAAAGGAGATCGTATAGGTTGATGATGATGATGATG 1438
QY 2326 GTTGTGTTTAACTGATGATGATGATGATGATGATGATGATGATGATGATG 2385
Db 1439 GTTGTGTTTAACTGATGATGATGATGATGATGATGATGATGATGATGATG 1498
QY 2386 CAGAGAACATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2445
Db 1499 GAGAGAACATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1558

QY 2446 TTCTTCTAAT 2457
Db 1559 CACCATGCGTT 1570

RESULT 4
US-08-868-373-13
; Sequence 13, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Javoriski, Jan G.
; APPLICANT: Post-Beltemiller, Martha A.
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868,373
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-08-868-373-13

Query Match 10.2%; Score 283.2; DB 4; Length 1548;
Best Local Similarity 55.5%; Pred. No. 2e-53;
Matches 723; Conservative 0; Mismatches 423; Indels 156; Gaps 3;

QY 1133 GTTCATAGACTAGGAGAAATCAGGAGAGTGTGACGAGAGACACTGCTTCAAGAA 1192
Db 396 GTTCATAGACTAGGAGAAATCAGGAGAGTGTGACGAGAGACACTGCTTCAAGAG 455
QY 1193 GAGATCTTAAAGCTGAGCATAGGAGAGAGAGACATACCTCCAGATCATCTTTC 1252
Db 456 CAGATCTTAAAGCTGAGCATAGGAGAGAGAGACATACCTCCAGATCATCTTTC 515
QY 1253 ATGAGAAACATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1312
Db 516 TGTTCACAG 575
QY 1313 AGCACTAG 1372
Db 576 TGTCTTAAATTAACCTTTCGCTTAACTAATGATGAAACAAAGATATGAAATCCTGT 635
QY 1373 GGTATAGCTGATTTTCAACCGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1432
Db 636 TGTGATATGATCTTCTTAACTTCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 695
QY 1433 CAAGTAG 1492
Db 696 TAAAGTAG 755
QY 1493 CATAGCTATGATCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1552
Db 756 TATGCTGCTGATCTTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 815
QY 1553 TGTAGTAG 1612
Db 816 TGTATCTACTAG 875
QY 1613 ACCTAATGTTCTTATAG 1672
Db 876 ACCGATGCTGTTTGTGAG 935
QY 1673 CTTCGCAATCTAAGTACCTGTCGAGACATTTGCTGCAATGATGATGATGATGATGATG 1732
Db 936 CAAAG 995
QY 1733 CCGTAGCTTCAAGTTTCAATTTTGTATTAATGCTTTTAAATCTCTTGAACGAC 1792
Db 996 ----- 995

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1793 TAGTAACAAATTTGTGTGTTTGTAGAGTGTGTACAGGAGAGATGAACAAGATT 1852
Db 996 -----TAAAGTTTCCGTTGTGTGTATATCAGAGAGAGATGTACAGGAG 1040
QY 1853 CAAGGGGTGAAGATGAAGAGACTTAATGAAGTTGAGAGTGAAGCTTCAAGACAA 1912
Db 1041 AACGGGGTTTGTGTGTGAAGATTAATGGCATTCAGAGGAACTCTCAAAACCA 1100
QY 1913 CATACACTTGTAGTCTCTGTGTCTTCTTCCAGAGCTTCTTCTTGTGTCG 1972
Db 1101 TATCACTACATGTGGTCTCTGTGTCTTACCATTAAGTAGAGAGATTTCTCTTT 1155
QY 1973 TTTCCTCGCGAGACATTCACCTGCGCCAAAACGTCACAAACACTTCTCTCTAC 2032
Db 1156 -----ATGACTCTAGTTGTGAAGAGCTTTTAAAGGTAAAGTAAACGTA 1202
QY 2033 TTCCGCCACGCAAAAACCAATGAATCAAGTCTTCTTCCAGTCTTCCAGCCATA 2092
Db 1156 -----ATGACTCTAGTTGTGAAGAGCTTTTAAAGGTAAAGTAAACGTA 1202
QY 2093 CATCCCGACTACAGTCTGCTTCGACATTTTGTCTCCAGCGGCAACAAAGTACT 2152
Db 1203 TATCCCGATTTTCAAACTGTGCTTCGACATTTCTGTATCCATCTGTGTGAAGGCTGT 1262
QY 2153 GCTTGAAGAGCTTCAAAAAGATCTAGGCTTGAAGAGATTAAGAGATTAAGAGAT 2212
Db 1263 GATGATGATGATTAAGAGAGATCTGACGCTTTCACCACTTATGTGAGGCTTGAAGAT 1322
QY 2213 GACACTTCAAGAGTTTGGAAACACTTGTAGAGTGAAGATGATGATGATGATGAT 2272
Db 1323 GACTCTTCACTGATTTGTGTATACATCTTGTGAGCTTGTATGATGATGATGATGAT 1382
QY 2273 GGAGGCCAAGAAAGTGTGTGTAGAGCGATAGAGGTTTGGCAGATCGTTTCTGCG 2332
Db 1383 TGAAGCCAAAGGAGATGCGAAGAGATTAATGCTTTGGCAAAATCGGCTTCGGAAGTGG 1442
QY 2333 TTTTAAATGTAAAGTGTGTGTGTGAAGGCAATGAGAAAGTGAAGAACCAACAGAA 2392
Db 1443 ATTAAATGTAAATGCGCGATTTGGAGAGCTTTAAAGCATGT-----GAAACCTTGAACAA 1499
QY 2393 CAATCTTGGGTGATTCATCAACCTTACCTGTGCTCT 2434
Db 1500 CAGTCTTGGGAGATGTATGTACAAAGTATCCGTACTTT 1541

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RESULT 5
US-08-066-299-10
Sequence 10, Application US/08066299
Patent No. 5445947

GENERAL INFORMATION:

APPLICANT: James George Metz
APPLICANT: Kathryn Dennis Lardizabal
APPLICANT: Michael W. Lassner
TITLE OF INVENTION: Fatty Acyl CoA: Fatty Alcohol
TITLE OF INVENTION: O-Acyltransferases
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/066, 299
FILING DATE: 19930520
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/796,256
FILING DATE: 20-NOVEMBER-1991
APPLICATION NUMBER: 07/933,411
FILING DATE: 21-AUGUST-1992
APPLICATION NUMBER: PCT/US92/09863
FILING DATE: 13-NOVEMBER-1992
ATTORNEY/AGENT INFORMATION:

NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845

NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 98

TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

LENGTH: 1733 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: CDNA to mRNA
US-08-066-299-10

Query Match 9.9%; Score 275.4; DB 1; Length 1733;
Best Local Similarity 54.6%; Pred. No. 1.1e-51;

Matches 729; Conservative 0; Mismatches 433; Indels 153; Gaps 3;

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QY 1126 AAGAAGATTATATGAACTAGACGAGAAATATAGGAGTGTGACGAGAGACACTCGGTT 1185
Db 424 ACGAGATTTCTATGACGAGGACGACCTCCGGCGGCTGTTTCTAAGAGAAATATTAGT 483
QY 1186 TCAGAGAGAGATCTTCAAGCCTTCAGCATAGCGAGAGACATATCGTCCAGATCCA 1245
Db 484 TTCAGAGAGAGATCTTCAAGAGGCGGCTATAGGTCGCGGAAACCTATGTCCTCCGATCCG 543
QY 1246 TCTCTTATCAAGAAACATTAACAAGATGAAGAAAGTGTGGAAGAGCTCTACAGTA 1305
Db 544 TCATTAAGGTGCGCCGCGGACGACATAGACAGCCAGAGGCGGAGGAGAGTGA 603
QY 1306 TCTTGGAGCACTAGACAGACCTTCTGAGAGACAGCTGTAAACCTTAAGAGCTTGGTG 1365
Db 604 TGTAAGGGGCGATGACAGAGGAGTGTGAAGAGAGGAGGAGTGAAGCCAGAGATAGGA 663
QY 1366 TCTTGTGTATACCTGTATGATTTCAACCCGACACCGTCTGTGCGCATGATGATTA 1425
Db 664 TACTGTGTGTGANTGACAGCTGTGTTAAACCAACCGCTGCTGTCATCATGATAGTTA 723
QY 1426 ACCATTCAAGATGAGAGGAGAAACATTAAGTATTAACCTTGAAGAGAGGATGTTGCG 1485
Db 724 ACCATTCAAGCTNAGGGGTATATTAATTAATTAATTAATTAATTAATTAATTAATTA 783
QY 1486 CTGGAATCATAGCTAATGATCTGTGCTGATGATGATGATGATGATGATGATGATGAT 1542
Db 784 CTGGGCTCATATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 843
QY 1543 ATGCGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1602
Db 844 ATGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 903
QY 1603 CAATGTTATACCTAATGTTCTTGTAGAGGTTGTTGCGGTTATGCTGCTTACAC 1662
Db 904 CCATGCTTATACCACTGCTTATTTCCATAGGTTGCGGCTGCTGCTGCTGCTGCTGCTGCT 963
QY 1663 GTCTGCTGATCTTGCCTCTAAGTACCTGCTGACATGCTGCTGCTGCTGCTGCTGCTGCT 1722
Db 964 GCTGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1023
QY 1723 CTGCTGACGACCGTATGCTTCAAGGTTTCATTCATTTGATTAATTCGTTTACATCTC 1782
Db 1024 GCGCTGACGAC----- 1034

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1783 TTGACCGACCTAGTAACTAATTTTGTGTGTTTAAAGAGTGTGTACAGGAAGATG 1842
1035 -----AGTCCATAGATGCGCTTACAAAGAAAGATG 1068
1843 AACAAAGATTCAAGGGGTTGAAGATAGTAGAGACTTAATGAGATGGAAGCTC 1902
1069 AAAATATACAAAGTAGGTGTGCTTATCCATAGAGATGAGATGGAGTGGCGGAAGCC 1128
1903 TCAGACAAACATCATACCTACCTAGTCTCTGTCTTCTTCTTCTTCTTCTTCTTCT 1962
1129 TAAAGGCCAAATCAGACAGCCTTGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1188
1963 TCTTGTCTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2022
1189 TCTTGTCTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1235
2023 CCTTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2082
1236 ----- 1235
2083 CCAAGCCATACATCCCGACTACAAAGCTGCTTGCAGATTTTGTCTTCCAGCGGCA 2142
1236 --AAGCCATACATCCCGACTACAAAGCTGCTTGCAGATTTTGTCTTCCAGCGGCA 1293
2143 GCAAACTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2202
1294 GCAAACTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1353
2203 CTTCTAGTATGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2262
1354 CTTCTAGTATGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1413
2263 TGGCTTACATGAGGCGCAAGAAAGTGTCTGAGAGCGATAGGCTTGTGCTGCTGCT 2322
1414 TGGCTTACATGAGGCGCAAGAAAGTGTCTGAGAGCGATAGGCTTGTGCTGCTGCT 1473
2323 TGGCTTACATGAGGCGCAAGAAAGTGTCTGAGAGCGATAGGCTTGTGCTGCTGCT 2382
1474 TGGCTTACATGAGGCGCAAGAAAGTGTCTGAGAGCGATAGGCTTGTGCTGCTGCT 1533
2383 CAAACGAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2442
1534 CTAAGAGAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1593
2443 TCATTTCTTCTAAT 2457
1594 TCGACACTATGCTT 1608
Db

RESULT 6
US-08-265-047-2
Sequence 2, Application US/08265047
Patent No. 5679881
GENERAL INFORMATION:
APPLICANT: Metz, James G.
APPLICANT: Lardizabal, Kathryn D.
APPLICANT: Lasserer, Michael
TITLE OF INVENTION: Nucleic Acid Sequences Encoding a Plant Cytoplasmic Protein
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,047

FILING DATE: 23-JUN-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/160,602
FILING DATE: 30-NOV-93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/796,256
FILING DATE: 20-NOV-91
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/933,411
FILING DATE: 21-AUG-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/066,299
FILING DATE: 20-MAY-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09863
FILING DATE: 13-NOV-92
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 101-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1733 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-265-047-2

Query Match 9.9%; Score 275.4; DB 1; Length 1733;
Best Local Similarity 54.6%; Pred. No. 1.1e-51;
Matches 729; Conservative 0; Mismatches 453; Indels 153; Gaps 3;

1126 AAGAGAGTTCATAGACATGACGAAATTCAGGAGTTCGACGAGACATCGGTT 1185
424 ACGAGATGTTTCATGACCGGACCTCCGGGCGGTCTTCTTAAGAGAAATATGAGT 483
1186 TCAAGAGAGATCTTCAAGGCTCAGCATAGGCGACGACATCGTCCCAAGTCCA 1245
484 TTCAGAGAGATCTTGAAGAGGCGGTGAGTGGTGGGAACCTATGTCGCCGAATCCG 543
1246 TCTCTTCATCAGAAACATATACAGATGAAAGAGTGTGTAAGAGCTTACAGTGA 1305
544 TCACATAGGTGCGCGCGGAGCGAGCATAGACACAGGCGCGGAGGAGAGTGA 603
1306 TCTTTGAGCCTAGACGAACTCTTGAAGAGACACGTGTAAACCTAAAGAGCTTGTG 1365
604 TGTACGGGCGGATCGACGAGGTGTGAGAGACGCGGGGTGAAGCCGAGAGATAGGA 663
1366 TCTTTGAGTAACTGATCATTTTCAACCGACACCGTCTGTCGCCGAATGCTATA 1425
664 TACTGTGTGAGACGACCTGTTTAAACCAAGCGGTGCTATCATGATATGTTA 723
1426 ACCATTAACAAGATGAGAGGAGACATATTAGTACAACTTGGAGGATGGATGTTCCG 1485
724 ACCATTAACAAGCTAGAGGATATATCTTATAGCATATATCTTGGTGCATAGGTTG 783
1486 CTGGAATCATATGATATGATCTTGTCTGAGACATGCTTACCTTAAATGTT 1542
784 CTGGGCTCATTTTCATGATCTTGGCAAGAGACCTCTTACAGGTTTACCTAAACAT 843
1543 ATGCTGTTTGTGAGTACTGAGATGTTGGGATATATGCTAGACGAGAGTGAAGT 1602
844 ATGTGTTAGTAGACACGAGAAACATGACCTTAAATGTTAGTGGGCAATGACCGCT 903
Db

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OY 1603 CAATGTTATACAAATGTTCTTTAGATGGGTTGTTGCCGTATGCTCTACACC 1662
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DB 904 CCAATGTTATACAAATGTTCTTTAGATGGGTTGTTGCCGTATGCTCTACACC 963
OY 1663 GTCGTGCTGACTTGGCCATGCTAAGTACCGCTGCGACATTTGCCAACTCAAG 1722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 964 GCTGGCGTATGTCGGCGGATCCAAAGTACCAATCTCTCATACAGTACGACCCAAAG 1023
OY 1723 CTGCTGACGACCGTACGTTCAAGTTTCAATTTGTTATTTATTTGTTTACAACTC 1782
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1024 GCGCTGACGAC----- 1034
OY 1783 TTGACCGACCTAATTAATTTTGTGTGTTTGAAGTGTGTACAGGAAGAAGAT 1842
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1035 -----AAGTCTATAGATGGCTTTTACACAGGAAGAAG 1068
OY 1843 AACAGATTCAGAGGGTTGAAGATTAAGTACAGCTTAATGGAAGTGAAGTGAAGTGC 1902
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1069 AAAATTAACAGTAGTGTGCTTATCCAAAGATCTGATGGCACTTGCCGTTGAAGCCC 1128
OY 1903 TCAAGACAAATCATCTACCTTAGTCTCTTGTCTCTACCTTTCTCCGACAGCTTCT 1962
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DB 1129 TAAAGGCCAATCATCAGCAGCTTGTGCTCCCTGCTGCTCCCATGTCAAGAACACTCTCT 1188
OY 1963 TCTTGTGCTTGTGCTCCGACCAATCTCAACCTGCTGCCAAAGCTCCAAACCACTT 2022
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DB 1189 TCTTGTGCTTGTGCTCCGACCAATCTCAACCTGCTGCCAAAGCTCCAAACCACTT 1235
OY 2023 CTTTCTACTTCTCCGCCACCCCAAAACCAATGGAATGATCTCTCTCCGATCTGT 2082
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DB 1236 ----- 1235
OY 2083 CCAAGCCTATATCCCGGACTACAAGCTCGCTTGACATTTTGTCTTCCAGCGGCA 2142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1236 --AAGCCTATATCCCGGACTACAAGCTCGCTTGACATTTTGTCTTCCAGCGGCA 1293
OY 2143 GCAAGTATGCTTGAAGAGCTTCAAAAGAACTCTAGGCTTGAGTAAGAAAGATATAGAG 2202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1294 GCAAGAGCTGTGATGATAGCTCGAAGAACTTGAGTTCAGGACGACCTTGAAC 1353
OY 2203 CTCTAGATGACACTTCAAGGTTTGAACACTTCTAGAGTGAAGTCTGTGTAGAT 2262
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1354 CCTGAGATGACACTGATATAGGTTTGGGAACACATGAGTCAATTAATGATGAGAT 1413
OY 2263 TGGCTTACATGAGAGCCCAAGAAAGTGTCTAGAGGCGATAGGTTTGGCAGATCGCT 2322
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1414 TGGCATAGCTGAAGCAAAAGGAGGATCCGTAAGGCTGATGAACTTGATGAT 1473
OY 2323 TCGGTTGCTTGAAGGTGAAGAGTGTGTGTTGGAAGCAATGAGGAAGGAAGC 2382
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1474 TTGGTTAGGTTTCAAGGTATACAGTGTGTGTGAGGAGCTTGTGAGGTGCAATCCGG 1533
OY 2383 CAACAGGAAACATCTTGGGTGATGATCAACCCGTGCTGCTCTAAATTA 2442
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1534 CTAGAGAGAAATCCTTGATGATGAATTAAGAAATTCCTGCTGATGCTTAA 1593
OY 2443 TCATTTCTTAAT 2457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1594 TCGCACCTATCGCT 1608
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 7
US-08-926-522-21
; Sequence 21, Application US/08926522
; Patent No. 6426447
; GENERAL INFORMATION:
; APPLICANT: Vic C. Knauf
; APPLICANT: Gregory A. Thompson
; TITLE OF INVENTION: PLANT SEED OILS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.

```

```

STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1(a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,522
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,173
FILING DATE: 2-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schmedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE DES
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1733 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-926-522-21

Query Match 9.9%; Score 275.4; DB 4; Length 1733;
Best Local Similarity 54.6%; Pred. No. 1.1e-51;
Matches 729; Conservative 0; Mismatches 453; Indels 153; Gaps 3;

OY 1126 AAGAAGAGTTCATAGACATAGCGAGAAATACAGGAAGTTGCGACGAGACCTCGTT 1185
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 424 ACGAGATGTTATAGACCGGACCTCCCGCGCGGCTGTTTCTAAGGATATATTGAGT 483
OY 1186 TCAAGAAAGATCTTACAGGCTTACAGCATAGGCGACGACATACGTTCCCAAGATCA 1245
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 484 TTCAAGAGAAAGATCTTGAAGAGGCGCGGATGCTGCGGAAACCTATGTCGCCGATCCG 543
OY 1246 TCTCTTCAAGAAATACATACAGATGAAGAGTCTGTAAGAAAGCTCTACAGTGA 1305
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 544 TCATTAAGGTGCGCGCCGACCGGACATAGCAGCGACGCGGCGGAGAGGTGA 603
OY 1306 TCTTTGAGACATAGACAACTCTTGAAGACAGCTGTAAACCTTAAGAGCTTGTG 1365
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 604 TGTAGGGGCGATTCACAGAGTGTGTGAAGAACGGGGGTGAAGCGGAAGCATAGGA 663
OY 1366 TCTTTGAGTAACTGTACATTTTCAACCGACACCGTGTGTCGCAATGTGATGA 1425
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 664 TACTGTGTGANTGACGCTGTGTTAACCCACCGCGCTGTCATCCATGATAGTTA 723
OY 1426 ACCATTACAGATGAGAGGAACATCTTATGTTACACCTTGAGAGGATGGATGTTGG 1485
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 724 ACCATTACAGATGAGAGGAACATCTTATGTTACACCTTGAGAGGATGGATGTTGG 783
OY 1486 CTGAATCATAGCTATGATCTTGTGCTGATGACATGCTTCAAGTAACTT--AATAGTT 1542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 784 CTGGGCTCATTTCCATGATCTTGTGCAAGAGACCTCTTACAGGTTTACCGTAAACACAT 843
OY 1543 ATGCTGTTGTGTGAGTACTGAGATGTTGGGTATTAATTTGATGCTGAGGATGCAAGT 1602
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 844 ATGTGTAGTAGAGACAGGAAACATGACCTTAATTTGATGCTGAGGATGACCGCT 903
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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OY 1603 CAATGTTATACCTAATTTCTTTAGAGATGGTGTCTGCGCTTATGCTTAACC 1662
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 904 CCAATGCTATACCACTGCTATTTGCGATGGTGGCGCTGCATCATCTCTCAAAC 963
OY 1663 GTCCGCTGACTTGGCCATGCTAAGTACCGTCTGAGACATTTGCCAATCAATAG 1722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 964 GCTGGGTATGCTGCGCCATCCAAAGTACCAACTCTTATACAGTACGACCCACAAG 1023
OY 1723 CTGCTGACGACCGTACCTTCAAGTTTCATTCATTTGGATTAATTCGTTTACAATCTC 1782
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1024 GGGCTGACGAC----- 1034
OY 1783 TTGACCGACCTAGTAATTTTGTGTTTGTAGAGTGTGTACGAGAGAGATG 1842
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1035 -----AAGTCTATAGATGCGCTCTTACAAAGAGATG 1068
OY 1843 AACAGGATTCAGGGGTTGAAGATTAAGTAACTTAATGGAAGTTGGAGTGAAGCTC 1902
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1069 AAAATACAGAGTATGTTGCTTATCCAGATCTGATGAGCATGTCGGGTGAAGCCC 1128
OY 1903 TCAGAGCAAAACATCACTACCTTAGGTCCTGCTACCTTCTCCGAGCAGCTTCT 1962
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1129 TAAAGGCCAATCAACAGACCTTGTGCTGCTGCTCCCATGTACAGAACATCTCT 1188
OY 1963 TCTTGTGCTTGTCTGCTGCGGACATCTCTACCTGTGCGCAAAAGTCCAAACCACTT 2022
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1189 TCTTTGCCACCTTACTGACAGCTAAGTCTTCAAGATGACAAAGCTG----- 1235
OY 2023 CTTTCTACTTCCGCGCACCGCAAAACCAATGGAATCAAGTCTTCTCCGATCTGT 2082
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1236 ----- 1235
OY 2083 CCAAGCCATACATCCCGACTACAGCTCGCTTCGACATTTTGTTCACGCGGCA 2142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1236 --AAGCCATACATCCCAATTTCAAGTGGCAGCAGACACTTCTGCAATCCATGCAAGAG 1293
OY 2143 GCAAGTGTGCTTGAAGAGCTTCAAAAGAACTAAGGCTTGAAGTGAAGATATGAGG 2202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1294 GCAAGGAGTGTGATGAGCTCGAGAGAACTTGAAGTGAAGCAGCAGTGGCACTTGAAC 1353
OY 2203 CTTTAGAGTACACTTACAGGTTTGAAGACATCTTACAGTGTGAATCTGTATGAGT 2262
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1354 CTTGAGGATACACTGTATAGTGTGGAGACACATCGAGTATGCTAATTAATGCTACGAGT 1413
OY 2263 TGGCTTACATGAGGAGCCAGGAAGTGTCTAGAGGAGATAGGTTTGGAGATCGCTT 2322
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1414 TGGCATACGCTGAAGCAAAAGAGAGATCCCTAAGGATGATGCAATTTGATGATGAT 1473
OY 2323 TCGGTTTCTGTTTAAGTGAAGTGTGTGTGAAGCAATGAGAAAGTGAAGAAAGC 2382
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1474 TTGGTTAGGTTTCAAGTGTAAAGTGTGTGTGAGGAGCTTTGAGGAGTCAATCCG 1533
OY 2383 CAACGAGAACATCTTGGTGGATGTGATCAACCGTACCGTGTGCTCTTAATTA 2442
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1534 CTAGAGAGAAAGATCTTGGATGATGAATGAGAAAGTCCCTGTCCATGTGCTTAAA 1593
OY 2443 TCATTTCTTAAT 2457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1594 TCGCAGCTATCGCTT 1608
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 8
US-08-868-373-1
; Sequence 1, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868,373
; CURRENT FILING DATE: 1997-06-03

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; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-08-868-373-1

Query Match      9.7%; Score 269; DB 4; Length 1560;
Best Local Similarity 55.2%; Pred. No. 2.7e-50;
Matches 723; Conservative 0; Mismatches 430; Indels 156; Gaps 4;

OY 1123 CAAGAGAGATTCATAGATAGCGAGAAATCAGGAAGTTGACGAGAGACACTCG 1182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 392 CAGTATGCTGCTTCTGAGATGACTGAGAAATATGATCATTCACCATGACAGGTTTC 451
OY 1183 GTTTCAGAGAGAGATCTTCAAGGCTCAGCATAGCCACAGACATACGTCCTCAAGT 1242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 452 AGTTCCAGAGAGAGATCTGAAACCGGCGGTTGGAGACGAGATCTGCGCACGTCG 511
OY 1243 CCATCTCTCATCAGAAAAATACACGATGAAGAGTGTGAAGAGCCTCTACAG 1302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 512 GCATACCTTCAAGGCGCCCGGAAAGCTAATATGTACAGAGCAGTCCGAACTGAAGCCG 571
OY 1303 TCATCTTGGACACTAGACGACATCTTGTGAGAGACACGTGTAAACCTTAAGACGTTG 1362
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 572 TTATGTTGGAGACCTTATGATTCCTCTTCGAGAAAAACCGAATTAACCGCGCAAGTCG 631
OY 1363 GTGTCTTGTGTGATACGTATGATCTTCAACCGGACCGGCTGTGTCGGAATGTCGA 1422
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 632 GAATCTTGATAGTAACTGACAGCTTATTCATCCAGCGCTCTTATGAGGATGATCG 691
OY 1423 TAAACCATTAAGATGAGAGGAGGAAATACCTTAGTTACAACTTGGAGGATGAGATGTT 1482
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 692 TGAACCATTAAGATGAGAGAGAGACATCAAAAGTTACAACTGAGAGGAATGGTTGCT 751
OY 1483 CGGCGGAGATCATACCTATGATCTGTGCTCGGACATGCTTCACTTAACCTTAATGATT 1542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 752 CGGCGGAGATTAATCAATCAATCAATCTGCTTAACAACTCTCTTAACAAACCTTAATGCT 811
OY 1543 ATGCTGTGTTGTGAGTACTGATGATGATGTTGGTAAATTTGAGTGGAGTGAAGTCAAGT 1602
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 812 ACGCTGTGTGTAGAGACAGGAAAAATTAACCTTAATCTGTTACTTGGAAATGACCGGT 871
OY 1603 CAATGTTAATCTAATTTGTTCTTTAGATGGTGTGCTTCCGCTTAATGCTCTTAAC 1662
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 872 CAATGCTCTCTGCAATGCAATCTTCCGATGGGAGGAGTCCGATCTCTCTAAC 931
OY 1663 GTGCTGCTGACTTTCGCATGCTAAGTACGCTTCGACACATTTGTCGAATCTAATAGG 1722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 932 GCCGTCAAGACCGGAGAGAAAGTCAAGTACTGCTGTCTCAAGTGTCTGAACACATTAAG 991
OY 1723 CTGCTGACGACCTAGCTTCAAGTTCATTCATTTTGGTATTAATGCTTTTACAATCTC 1782
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 992 GATCAGACGACAAAGACTACATTT----- 1015
OY 1783 TTGACGACCTAGTAATTTTGTGTTTGTAGAGTGTGTACGAGAGAGATG 1842
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1016 -----GGGTGTACAGAGAGAGACG 1036
OY 1843 AACAGGATTCAGGGGTTGAAGTAAAGTAAAGATTAATGAAGTTGAGGTGAAGCTC 1902
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1037 AGAGAGAGAACATGCGTCTCTTACTAGAGGCTCATGCTGTGCGCGAGAACCTCG 1096
OY 1903 TCAAGCAAAACATCACTACCTTAGAGTCTTGTGCTACCTTCTGAGAGAGGTTCTCT 1962
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1097 TGAAGAAACATCACTACCTTAGAGACGATGTTCTTCCATTTGTCAGACAGATGTATGT 1156
OY 1963 TCTTGTGCTTGTGCTCCGCGGAGAACATTCACCTGCTGCCAAAGCTCCACAACCACTT 2022
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1157 TCTTGTATTCCTTGTGTC----- 1173
OY 2023 CTTTCTTACTTCCGCGCACCGCAAAACCAATGGAATCAAGTCTTCTCTCCGATCTGT 2082
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


TELECOMMUNICATION INFORMATION:

TELEPHONE: (503) 226-7391

TELEFAX: (503) 228-9446

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1491

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-09-058-947A-3

Query Match 8.9%; Score 247.4; DB 4; Length 1491;

Best Local Similarity 53.9%; Pred. No. 1.5e-45;

Matches 698; Conservative 0; Mismatches 441; Indels 156; Gaps 3;

QY 1134 TTTCATGAACTAGCGAGAAATCAGGAAAGTTGCGAGAGAGACTGGTTCAAGANG 1193
 DB 328 TTTCATGAACTAGCGAGAAATCAGGAAAGTTGCGAGAGAGACTGGTTCAAGANG 387
 QY 1194 AGGATCTTACAGCGCTGAGGCGATGAGGCGAGACATAGCTCCCAAGATCCATCTCTCA 1253
 DB 388 AAGATCTTACAGCGCTGAGGCGATGAGGCGAGACATAGCTCCCAAGATCCATCTCTCA 447
 QY 1254 TCAGAAACATTAACAAGATGAAAGAGTGTGAAGAGAGCTCTACAGTGAATCTTGA 1313
 DB 448 ATTCCTCCACACCAACCATGAGAGCGGCTAGAGAGGAGCTCAGATGTTATCTTCGAG 507
 QY 1314 GCACATGAGAGAGCTCTGAGAGAGAGCTGTAAGAGAGCTGTAAGAGAGCTGTAAG 1373
 DB 508 GCACATGAGAGAGCTCTGAGAGAGAGCTGTAAGAGAGCTGTAAGAGAGCTGTAAG 567
 QY 1374 GTTAAGTGAAGATTTTCAACCGGACCGCTGCTGCGCAATGGTATTAACCATTTAC 1433
 DB 568 GTTAAGTGAAGATTTTCAACCGGACCGCTGCTGCGCAATGGTATTAACCATTTAC 627
 QY 1434 AAGATGAGAGGAGACATTAATTAACAACCTTGAAGAGAGTGGATGTTGCGCTGGAATC 1493
 DB 628 AAGATGAGAGGAGACATTAATTAACAACCTTGAAGAGAGTGGATGTTGCGCTGGAATC 687
 QY 1494 ATAGCATTTGATCTGCTGCTGAGACATGCTTCAAGTCAATTAAGTATGTTGTT 1553
 DB 688 ATAGCATTTGATCTGCTGCTGAGACATGCTTCAAGTCAATTAAGTATGTTGTT 747
 QY 1554 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1613
 DB 748 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807
 QY 1614 CCTAATGTTTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1673
 DB 808 CCTAATGTTTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 867
 QY 1674 TTTCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1733
 DB 868 TTTCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 927
 QY 1734 CGTAGCTTACGTTTCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1793
 DB 928 CGTAGCTTACGTTTCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 927
 QY 1794 AGTAACTAATTTTGTGTTTGAAGATGATGATGATGATGATGATGATGATGATGATGAT 1853
 DB 928 AGTAACTAATTTTGTGTTTGAAGATGATGATGATGATGATGATGATGATGATGATGAT 922
 QY 1854 AAGGGTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1913
 DB 973 GTTGGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1032
 QY 1914 ATCACTACCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1973
 DB 1033 ATCACTACCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1092
 QY 1974 TTGCTCCGCGAATTTCTACCTGCTGCGAAAGAGTCCACCAACCACTTCTCTCTACT 2033

DB 1093 CTAATCGAGCTTAAT----- 1109
 QY 2034 TCCGCCACCGCAAAAACCAATGATCAAGTCTTCTCCGATCTGTCCAAAGCCATAC 2093
 DB 1110 -----CTTCACCCGAAATGGAACCATAC 1134
 QY 2094 ATCCGAGCTACAGCTGCGCTTGCAGATTTTGTCTCCAGCGGCAAGAAATGATG 2153
 DB 1135 ATACCGGATTTCAAGCTGCGCTTGCAGATTTTGTCTCCAGCGGCAAGAAATGATG 1194
 QY 2154 CTTGAAGAGCTTCAAAAAGATATGAGCTTGAAGAGAGAAATGAGAGCTTCTAGATG 2213
 DB 1195 ATGAGAGAGCTTCAAAAAGATATGAGCTTGAAGAGAGAAATGAGAGCTTCTAGATG 1254
 QY 2214 ACACCTTCAAGCTTGAAGAGAGCTTGAAGAGAGAAATGAGAGCTTCTAGATG 2273
 DB 1255 ACACCTTCAAGCTTGAAGAGAGCTTGAAGAGAGAAATGAGAGCTTCTAGATG 1314
 QY 2274 GAGGCCAAGAAAGTGTGATGAGGAGATGAGGCTTGGCAGATGCTTGGTCTGCTG 2333
 DB 1315 GAGCTTAAGAGGAGATGAGAGAGGAGATGAGGCTTGGCAGATGCTTGGTCTGCTG 1374
 QY 2334 TTTAAGTGAAGAGTGTGATGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 2393
 DB 1375 TTTAAGTGAAGAGTGTGATGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 1431
 QY 2394 ATCTCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2428
 DB 1432 GAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1466

RESULT 12
 US-09-058-947A-2
 ; Sequence 2, Application US/09058947A
 ; Patent No. 6274790
 ; GENERAL INFORMATION:
 ; APPLICANT: Kunst et al.
 ; TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
 ; TITLE OF INVENTION: Involved In Very Long Chain Fatty Acid Synthesis
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klarquist Sparkman Campbell
 ; ADDRESSEE: Leigh & Whinston, LLP
 ; STREET: One World Trade Center, Suite
 ; STREET: 1600, 121 S.W. Salmon Street
 ; CITY: Portland
 ; STATE: OR
 ; COUNTRY: USA
 ; ZIP: 97204-2988
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Disk, 3.5-inch
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: Windows NT
 ; SOFTWARE: Word97 & ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/058,947A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/043,831
 ; FILING DATE: April 14, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: David J. Earp, Ph.D.
 ; REGISTRATION NUMBER: 41,401
 ; REFERENCE/DOCKET NUMBER: 5493-50032/DJE
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (503) 226-7391
 ; TELEFAX: (503) 228-9446
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1807
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double

TOPOLOGY: linear
US-09-058-947A-2

Query Match 8.9%; Score 247.4; DB 4; Length 1807;
Best Local Similarity 53.9%; Pred. No. 1,6e-45;
Matches 698; Conservative 0; Mismatches 441; Indels 156; Gaps 3;

QY 1134 TTCATAGAACTAGCGAATAATCAGGAAAGTTCGACGAAAGACACTCGCTTCAAGANG 1193
DB 386 TTCAAGAACTAGCTGCTGTTGATCCCTCAAGGACAAAGCCCTTAAGAGGCTGAGTCCAAAG 445
QY 1194 AAGATCTTACAAAGCCCTAGGCGATAGCGACGACATACGCTCCCAAGATCCATCTCTTCA 1253
DB 446 AAGATCTTGAAGCTTGGCCCTCGGTGAGAGACTTGTCTCCCTCCGCTTATCTATT 505
QY 1254 TCAGAAACATPACACGATGAAAGAGTGTGAAGAACCTCTACAGTGTCTTGA 1313
DB 506 ATTCTCCACACCAACCATGAGCGCGCTAGACGAGCTCAGATGTTATCTTCGAG 565
QY 1314 GCATAGAGCACTCTGGAGAGACAGTGAACCTTAACCTTAAGAGCTTGTCTCTG 1373
DB 566 GCATAGAGCACTCTTTCAGAAACCGGTCTTAACCTTAAGAGCTGACATCTTATC 625
QY 1374 GTTAAGTGTAGCTTTTCAACCCGACACCGTGTGTCGCAATGATGTAACCATTC 1433
DB 626 GTCAAGCTGCTCTTTCTCTCCACACCATGCTCTCAGCTATGCTCATCAACAATAT 685
QY 1434 AAGATGAGAGGACATCTTACTTACAACTTGGAGGAGTGGATGTTGCGCTGGAATC 1493
DB 686 AAGCTTAGAGTAAATATCAAGAGCTTCAATCTTGGGATGGCTGACGCGGCGCTG 745
QY 1494 ATAGTATGATCTTGTGCTGACATGCTAGCTCACTAACCTTAACCTTAAGTATCTCTGTT 1553
DB 746 ATCTAGATGATCTTACCGCGAGCTGCTCAAGTCTCAATCCCAATTCACCAATCAATC 805
QY 1554 GTGAGTACTGATGTTGGGATTAATGATGATGAGAGAGTGAACATCAATGTTTAA 1613
DB 806 GTCAAGCAGGAGATCATTAACGCTTAATACATCAAGCAGACAGAGAGCCATGTTGTTA 865
QY 1614 CCTAATTTCTTTAGTAGAGTGGTGTGCTGCTTATGCTCTTACCGCTGCTGAC 1673
DB 866 CCCAATGCTCTTCCGAGTGGGTGCGGACCATATACATGCTCAACCGCGGCTGAC 925
QY 1674 TTTGGCATTGCTAGTACGCTCGAGCAATGTCGCAACTCATTAAGGCTGCTACAC 1733
DB 926 CGGTGGCAGCCAAATTAACCTTCCACCTCGTCCGACACACCGTGGCTGACAC 985
QY 1734 CGTAGCTTACAGTTTCAATTTGATTAATTCGTTTACATCTCTGACGACCT 1793
DB 986 ----- 985
QY 1794 AGTAATTAATTTGTGTGTTTAAAGAGTGTGACGAGAGAGATGAACAGATTC 1853
DB 986 -----AAGTCTTCTACTGTCTCTACGAAACAGAGAAAGAGAGACAC 1030
QY 1854 AAGGGTTGAGATTAAGATGAGACTTAATGGAAGTGGAGTGAAGCTCTCAAGCAAC 1913
DB 1031 GTTGGCATCAACTGTCCAAAGATCTCAATGCGCATGCGGCTGAAGCCCTCAAGCAAC 1090
QY 1914 ATCACTAATGCTGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1973
DB 1091 ATCAACCAATTAAGTCT 1150
QY 1974 TTGCTCGGCGAATCTCTACCTGCTGCGCAAAAGCTCCACACCATCTCTCTCTACT 2033
DB 1151 CTAAATCGAGCTAAAT----- 1167
QY 2034 TCCGCAACCGCAAAACCAATGAATCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2093
DB 1168 -----CTTCAACCGCAAAATGGAACCAATAC 1192
QY 2094 ATCCCGAGTACAGATCGCTGCTGAGCAATTTGCTTCCACGCGGCAAGCAAGATGAGT 2153
|| ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 1193 ATACGGATTTCAAGCTGCTTTCGACACTTTTGCATTCACGACAGAGACAGCGGTG 1252
QY 2154 CTGGAAGCTTCAAAAGATCTAGGCTGAGTGAAGAGATATGAGGCTTCTAGATG 2213
DB 1253 ATCGAGAGACTCCAAAGATCTACAACTATCAAGGAAACAGCTTGAAGGCTTCAAGATG 1312
QY 2214 ACATCTACAGGTTTGGAAACCTTCTACAGTGAAGTGTGTATGAGTGTGCTTACATG 2273
DB 1313 ACATCTACAGTGTGTTGGTGAACGCTCATCTCTATGATGATGAGCTTATGCTATC 1372
QY 2274 GAGGCAAGGAAGTGTGAGAGCGATAGGCTTGGCAATGCTTTCGCTTCTGCT 2333
DB 1373 GAGCTTAAAGGAATGAGAGAGCGATGCGTGGCAATGCGCTTGGAGTGTG 1432
QY 2334 TTTAAGTGTACAGTGTGCTGAGAGCAATGAGAGAGTGAAGGCAAGCAACAGAGAC 2393
DB 1433 TTCAAGTGTACCTGCGCTGTGGAATTAATACCGTACATTAAGA---CACTTAAGAC 1489
QY 2394 AATCTTGGGTGATTCATCAACGTTTACCTGT 2428
DB 1490 GGACCATGCTCCGATGTTATCGACCGTTCCTGT 1524

RESULT 13

US-09-058-947A-1
Sequence 1, Application US/09058947A

Patent No. 6274790

GENERAL INFORMATION:

APPLICANT: Kunst et al.

TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klariquist Sparkman Campbell

STREET: One World Trade Center, Suite

CITY: Portland

STATE: OR

COUNTRY: USA

ZIP: 97204-2988

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk, 3.5-inch

OPERATING SYSTEM: Windows NT

SOFTWARE: Word97 & ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/058, 947A

FILING DATE:

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/043, 831

FILING DATE: April 14, 1997

ATTORNEY/AGENT INFORMATION:

NAME: David J. Bair, Ph.D.

REGISTRATION NUMBER: 41,401

REFERENCE/DOCKET NUMBER: 5493-50032/DJE

TELECOMMUNICATION INFORMATION:

TELEPHONE: (503) 226-7391

TELEFAX: (503) 228-9446

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3722

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-09-058-947A-1

Query Match 8.9%; Score 247.4; DB 4; Length 3722;

Best Local Similarity 53.9%; Pred. No. 2e-45;

Matches 698; Conservative 0; Mismatches 441; Indels 156; Gaps 3;

QY 1134 TTCATAGAACTAGCGAATAATCAGGAAAGTTCGACGAAAGACACTCGCTTCAAGANG 1193

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Db 2279 TTCTGGAACACCTCTCTTTGATTCCTCAAGACCAAGCCTTAGAGCTGAGTTCCTCAATG 2338
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Qy 1194 AGATCTTACCAAGCTTACGACATAGCGACGACATACGTCCCAAGATTCATCTTCA 1253
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Qy 1254 TCANAAAACATTAACAGATGAAGAAGTCTGTGAAGAAGCTCTACAGTATCTTTGGA 1313
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Db 2399 ATTCTCCACACCAACACATGACGCGGTAGAAAGCGAGCTCAGATGTTATCTTCAG 2458
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Qy 1314 GCACCTAGACGAACTCTTCGAGAGACAGTGTAAACCTTAAGAGCTTGGTCTCTTG 1373
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Db 2459 GCCATGAGACGATCTTTCCAGAAAACCGGTCTTAACCTTAAGAGCTGACATCTTATC 2518
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Db 2519 GTCAACTGCTCTCTTTCTCTCCACACATCGCTCAGCTAGTATGATCAACAATAT 2578
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Qy 1434 AAGATGAGGAGACATCTTATTAACACTTGGAGGATGGATGTTCCGCTGGAAATC 1493
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Db 2579 AAGCTTAGAGATTAATACAGAGCTTCAATCTTCGGGATGGCTGCAGCGCGGCTG 2638
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Qy 1494 ATACCTATTGATCTTGTCTGACATGCTTCACTTAACCTTAATAGTATGCTGTGTT 1553
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Qy 1554 GTGAGTCTGAGATGTTGGGTAAATTTGTAAGTGGAGATGACAAAGTCAATGTTATTA 1613
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Db 2699 GTTCGACGAGCATATACGCCCTTAATTAATCAAGCAAGAGAGCATCTTTGTTA 2758
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Qy 1614 CCTAATGTTCTTATAGATGGGTTTGTCTGCGTAAATGCTTAACCCGCTGCTGAC 1673
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Qy 1854 AAGGGTTGAAGATTAAGTAACTTAATGAGATGAGTGAAGCTCTCAACAAC 1913
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Qy 1914 ATCACTACCTTGAAGTCTCTGTGCTTCTTCCGAGACGCTTCTCTTGTGCT 1973
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Db 2984 ATCAACCAATAGTCTCTTGTGCTTCCCGGCTCAGAACATCTCTCTCAACGCTCC 3043
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Qy 1974 TTGTCGCGGCAATCTCTACCTGTGTCGCAAAAGCTCAACACATCTCTCTACT 2033
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Qy 2154 CTGAAGAGCTTCAAAAGATCTAGGCTTGAAGAGATGAGAGGCTTCAAGATG 2213
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Qy 2214 ACACCTCAGAGTTGGAACACTTCTAGAGTGAATCTGTGATGAGTTGCTTACATG 2273
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Db 3206 ACACACTACGCTTTTGTGAACACGTCATCTTCATGCTATGATGACAGCTTAGCTACATC 3265
Qy 2274 GAGGCCAAGAAAGTGTCTGAGAGCGATAGAGTTTGGCAGATCCCTTTGGTCTGCT 2333
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Db 3266 GAGCTTAAGAGGAGATAGAGAGAGCGATCGCTTTGGCAAAATCGCTTTGGGAGTGT 3325
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Qy 2394 AATCCTTGGTGATTTGCATCAACCGTTACCTGT 2428
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Db 3383 GGACCATGCTCCGATTTGATGACCGCTTACCTGT 3417

RESULT 14
US-08-888-998-1
: Sequence 1, Application US/08888998
: Patent No. 6124524
: GENERAL INFORMATION:
: APPLICANT: JAMES, Douglas W.
: APPLICANT: LIM, Eda
: APPLICANT: KELLER, Janis
: APPLICANT: DOONER, Hugo K.
: TITLE OF INVENTION: FAEI GENES AND THEIR USES
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourile and Crew
: STREET: Steuart Street Tower, One Market Plaza
: CITY: San Francisco
: STATE: California
: COUNTRY: US
: ZIP: 94105-1493
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/888,998
: FILING DATE: 07-JUL-1997
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/329,603
: FILING DATE: 26-OCT-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Bastian, Kevin L.
: REGISTRATION NUMBER: 34,774
: REFERENCE/DOCKET NUMBER: 12176-004300
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 543-9600
: TELEFAX: (415) 543-5043
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1641 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: 1..1641
: OTHER INFORMATION: /product= "FAEI from Arabidopsis"
US-08-888-998-1

Query Match 7.5%; Score 210; DB 3; Length 1641;
Best Local Similarity 53.08; Pred. No. 2.6e-37;
Matches 664; Conservative 0; Mismatches 435; Indels 153; Gaps 4;
Qy 1177 CACTCGGTTCAAGAGAGATCTTACAGGCTCAGCATAGCGACGACGACATACGTC 1236
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Db 365 CGCTCGATTTCTGAGGAATCAAGAGCGTCTAGCTAGTGTGATGACGCTACAGCTC 424
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Result No.	Score	Query Match	Length	DB	ID	Description
1	2782	100.0	2782	10	US-09-905-657-1	Sequence 1, Appl1
2	1162	41.8	1653	9	US-09-938-842A-2597	Sequence 2997, Ap
3	1157.4	41.6	1650	10	US-09-883-797-7	Sequence 7, Appl1
4	792	28.5	811	10	US-09-770-445-774	Sequence 774, Appl1
5	283.2	10.2	1548	10	US-09-883-797-13	Sequence 13, Appl1
6	278	10.0	1587	9	US-09-938-842A-1598	Sequence 1598, Ap
7	273.8	9.8	1530	9	US-09-938-842A-1205	Sequence 1205, Ap
8	269	9.7	1560	9	US-09-883-797-1	Sequence 1, Appl1
9	269	9.7	1563	9	US-09-938-842A-1552	Sequence 1552, Ap
10	268.4	9.6	1611	10	US-09-883-797-9	Sequence 9, Appl1
11	249.6	9.0	409	10	US-09-878-574-4051	Sequence 4051, Appl1
12	249	9.0	1502	10	US-09-883-797-11	Sequence 11, Appl1
13	247.4	8.9	1491	10	US-09-892-325-5	Sequence 3, Appl1
14	247.4	8.9	1494	9	US-09-938-842A-569	Sequence 569, App
15	247.4	8.9	1807	10	US-09-892-325-2	Sequence 2, Appl1
16	247.4	8.9	3722	10	US-09-892-325-1	Sequence 1, Appl1
17	238.8	8.6	1735	10	US-09-877-476-5	Sequence 5, Appl1
18	229.6	8.3	1521	10	US-09-877-476-39	Sequence 39, Appl1
19	228.8	8.2	1521	10	US-09-877-476-21	Sequence 21, Appl1

20	228	8.2	1521	10	US-09-877-476-35	Sequence 25, Appl
21	228	8.2	1521	10	US-09-877-476-37	Sequence 37, Appl
22	227.6	8.2	1518	10	US-09-877-476-17	Sequence 17, Appl
23	227.6	8.2	1521	10	US-09-877-476-15	Sequence 15, Appl
24	227.6	8.2	1521	10	US-09-877-476-19	Sequence 19, Appl
25	227.6	8.2	1524	10	US-09-877-476-13	Sequence 13, Appl
26	227.2	8.2	1521	10	US-09-877-476-13	Sequence 13, Appl
27	226.4	8.1	1521	10	US-09-877-476-23	Sequence 23, Appl
28	226	8.1	1518	10	US-09-877-476-9	Sequence 9, Appl
29	226	8.1	1521	10	US-09-877-476-11	Sequence 11, Appl
30	226	8.1	1524	10	US-09-877-476-3	Sequence 7, Appl
31	225.6	8.1	1521	10	US-09-877-476-7	Sequence 7, Appl
32	222.8	8.0	1521	10	US-09-877-476-41	Sequence 41, Appl
33	221.2	8.0	1521	10	US-09-877-476-31	Sequence 31, Appl
34	213.2	7.7	1521	10	US-09-877-476-29	Sequence 29, Appl
35	210	7.5	1709	10	US-09-877-476-1	Sequence 1, Appl
36	210	7.5	1709	10	US-09-877-476-35	Sequence 35, Appl
37	206.4	7.4	1521	10	US-09-877-476-27	Sequence 27, Appl
38	206.2	7.4	1512	10	US-09-883-797-5	Sequence 5, Appl
39	189.2	6.8	1479	10	US-09-883-797-3	Sequence 3, Appl
40	177.4	6.4	387	10	US-09-878-574-1.1065	Sequence 1065, Appl
41	175	6.3	2000	9	US-09-938-8424-5275	Sequence 5275, Ap
42	173.6	6.2	343	10	US-09-878-574-2604	Sequence 2604, Appl
43	137.8	5.0	468	10	US-09-770-444-253	Sequence 253, Appl
44	134.6	4.8	1431	9	US-09-938-8424-1987	Sequence 1987, Ap
45	122.6	4.4	276	10	US-09-878-574-12488	Sequence 12488, Ap

ALIGNMENTS

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RESULT 1
US-09-905-657-1
Sequence 1, Application US/09905657
Patent No. US20020038471A1
GENERAL INFORMATION:
APPLICANT: BAYER AG
TITLE OF INVENTION: Use of VICEAE for identifying herbicidally
active compounds
FILE REFERENCE: Lg A 34 730
CURRENT APPLICATION NUMBER: US/09/905,657
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
Seq ID NO 1
LENGTH: 2782
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (176)..(583)
NAME/KEY: CDS
LOCATION: (1119)..(1745)
NAME/KEY: CDS
LOCATION: (1821)..(2438)
US-09-905-657-1

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Query Match	100.0%;	Score 2782;	DB 10;	Length 2782;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2782;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db	61	TAAACATGACATATTCATATTTTGGCAACAACGCTTATTAAGTATACA	120
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Db	121	CTTCATCACTATAGATCTCACTGCATCAATATCAACTACAAAACAAACAGATGGG	180

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1861 TGAAGATTAAGTACGCTTTCAGAGGCTGTACAGAGAGATTAATTAATTAATTAATTAATTAATTA 1920
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2101 ACTACAAGCTGCTGCTGAGATTTTCTGCTCCAGCGGCAAGCAAGTATGCTTGAAG 2160
2101 ACTACAAGCTGCTGCTGAGATTTTCTGCTCCAGCGGCAAGCAAGTATGCTTGAAG 2160
2161 ACCTTCAAAAGATCTAGGCTTGAAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 2220
2161 ACCTTCAAAAGATCTAGGCTTGAAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 2220
2221 AAGGTTTGAAGACCTTATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
2221 AAGGTTTGAAGACCTTATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
2281 AAGAAAGTGTGTGAGAGCGATAGGTTTGGACAGATCTTCTGCTTCTGCTTCTGCTTCTGCTT 2340
2281 AAGAAAGTGTGTGAGAGCGATAGGTTTGGACAGATCTTCTGCTTCTGCTTCTGCTTCTGCTT 2340
2341 GTTACAGTGTGTGTGAGAGCGATAGGATGAGAGCGAATCCAGAAATCTCTT 2400
2341 GTTACAGTGTGTGTGAGAGCGATAGGATGAGAGCGAATCCAGAAATCTCTT 2400

Db 2341 GTAAACGTGTGTGTGGAGGCAATGAGAGGTAAGAAAGCAACAGCAATCTT 2400
QY 2401 GGGGATGTCATCAACCGTTACCGTCTCTCTAAATATATCTTCTAAATTTAA 2460
Db 2401 GGGGGATTCATCAACCGTTACCGTCTCTCTAAATATATCTTCTAAATTTAA 2460
QY 2461 TCAAGTATGATCTCTATTAATCTCCAAACCAAGATACAGTTGGTGGATGAGATT 2520
Db 2461 TCAAGTATGATCTCTATTAATCTCCAAACCAAGATACAGTTGGTGGATGAGATT 2520
QY 2521 ATTTACTGATCAATTCGTATCTAAGTCGTATTAAGAAATGATGAGTGGTGGTTC 2580
Db 2521 ATTTACTGATCAATTCGTATCTAAGTCGTATTAAGAAATGATGAGTGGTGGTTC 2580
QY 2581 AGCTCACTGTTTATTTTGTGTCTCTATGATCTCTATTAATTTTGAAGA 2640
Db 2581 AGCTCACTGTTTATTTTGTGTCTCTATGATCTCTATTAATTTTGAAGA 2640
QY 2641 TTAAGAAAAAACTCTCTTATGATGATGATGATGATGATGATGATGATGATGAT 2700
Db 2641 TTAAGAAAAAACTCTCTTATGATGATGATGATGATGATGATGATGATGATGAT 2700
QY 2701 ATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
Db 2701 ATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
QY 2761 GTTACGTGTATAGAGATAC 2782
Db 2761 GTTACGTGTATAGAGATAC 2782

RESULT 2

US-09-938-842A-2597
; Sequence 2597, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: S01P1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2597
; LENGTH: 1653
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2597

Query Match 41.88; Score 1162; DB 9; Length 1653;
Best Local Similarity 94.38; P-Value 2.8e-230;
Matches 1247; Conservative 0; Mismatches 0; Indels 75; Gaps 1;

QY 1117 AGGTGACAAAGAGAGATCTATAGAACTAGCGAGAAATCAGGAAATGTCAGCAAGA 1176
Db 407 AGGTGACAAAGAGAGATCTATAGAACTAGCGAGAAATCAGGAAATGTCAGCAAGA 466
QY 1177 CACTGCTTCAAGAGAGATCTTACAGCCTCAGCAGATAGGCGAGAGACATACGCTC 1236
Db 467 CACTGCTTCAAGAGAGATCTTACAGCCTCAGCAGATAGGCGAGAGACATACGCTC 526
QY 1237 CAAGATCATCTCTCTATGAGAAACATACAGATGAGAAAGAGTCTGAGAGAGCT 1296
Db 527 CAAGATCATCTCTCTATGAGAAACATACAGATGAGAAAGAGTCTGAGAGAGCT 586

QY 1297 CTACAGTATCTTTGGAGCACTAGAGCACTCTGAGAAAGACAGTGTAAACCTAAG 1356
Db 587 CTACAGTATCTTTGGAGCACTAGAGCACTCTGAGAAAGACAGTGTAAACCTAAG 646
QY 1357 ACCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1416
Db 647 ACCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 706
QY 1417 TGTGATTAACCATTTACAGATGAGAGGAAACATCTAGTTACACCTTGGAGGATG 1476
Db 707 TGTGATTAACCATTTACAGATGAGAGGAAACATCTAGTTACACCTTGGAGGATG 766
QY 1477 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1536
Db 767 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 826
QY 1537 ATAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1596
Db 827 ATAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 886
QY 1597 ACAAGTCAATGCTTATACCTAATTTCTTTAGAGATGCTGCTGCTGCTGCTGCT 1656
Db 887 ACAAGTCAATGCTTATACCTAATTTCTTTAGAGATGCTGCTGCTGCTGCTGCT 946
QY 1657 CTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1716
Db 947 CTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1006
QY 1717 ATAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1776
Db 1007 ATAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1032
QY 1777 AATCTTTGACCGACCTAGTAACTAATTTGCTGCTTTTAGAGATGCTGCTGCTGCT 1836
Db 1033 AATCTTTGACCGACCTAGTAACTAATTTGCTGCTTTTAGAGATGCTGCTGCTGCT 1051
QY 1837 AAGATGAACAGATTCAGGAGGTTGAAGATTAAGTATGATGATGATGATGATGATGATG 1896
Db 1052 AAGATGAACAGATTCAGGAGGTTGAAGATTAAGTATGATGATGATGATGATGATGATG 1111
QY 1897 AAGCTCAAGCAACATCACTACCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1956
Db 1112 AAGCTCAAGCAACATCACTACCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1171
QY 1957 TTCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2016
Db 1172 TTCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
QY 2017 CCATCT 2076
Db 1232 CCATCT 1291
QY 2077 ATCTGTCACAGCCATATACCTCCGAGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCT 2136
Db 1292 ATCTGTCACAGCCATATACCTCCGAGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1351
QY 2137 CGGCAAGCAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2196
Db 1352 CGGCAAGCAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1411
QY 2197 TGAAGCTTCTAGATGATCACTTACAGGTTTGAACACTTCTAGCAGTGGATCTGCTGCT 2256
Db 1412 TGAAGCTTCTAGATGATCACTTACAGGTTTGAACACTTCTAGCAGTGGATCTGCTGCT 1471
QY 2257 ATGAGTTGCTTACATGAGGAGCAAGAAAGTCTCTAGAGGAGATGAGGTTTGGCAGA 2316
Db 1472 ATGAGTTGCTTACATGAGGAGCAAGAAAGTCTCTAGAGGAGATGAGGTTTGGCAGA 1531
QY 2317 TCGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2376
Db 1532 TCGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1591

QY 2377 AGAAGCCAAACAGAAACATCTGGGTGATTCATCAACCGTTACCTGTGCTCTCT 2436
 DB 1592 AGAAGCCAAACAGAAACATCTGGGTGATTCATCAACCGTTACCTGTGCTCTCT 1651
 QY 2437 AA 2438
 DB 1652 AA 1653

RESULT 3

US-09-883-797-7
 ; Sequence 7, Application US/09883797
 ; Patent No. US20020066123A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jaworski, Jan G.
 ; APPLICANT: Post-Belienmiller, Martha A.
 ; APPLICANT: Todd, James
 ; TITLE OF INVENTION: FATTY ACID ELONGASES
 ; FILE REFERENCE: 07148/064001
 ; CURRENT APPLICATION NUMBER: US/09/883,797
 ; CURRENT FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 08/868,373
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO: 7
 ; LENGTH: 1650
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-883-797-7

Query Match 41.6%; Score 1157.4; DB 10; Length 1650;
 Best Local Similarity 94.2%; Pred. No. 2.5e-229;
 Matches 1243; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 1117 AGTGCAAAAGAGAGAGTTCATGAACTAGCGAAGAAATCAGGAAAGTTGACGAGAGAGA 1176
 DB 407 AGGTGCAAAAGAGAGAGTTCATGAACTAGCGAAGAAATCAGGAAAGTTGACGAGAGAGA 466
 QY 1177 CACTGCGTTTCAAGAGAGATCTTCAAGCCGACGAGTAGGCGAGACATACGTCC 1236
 DB 467 CACTGCGTTTCAAGAGAGATCTTCAAGCCGACGAGTAGGCGAGACATACGTCC 526
 QY 1237 CAAGATCATCTCTTCATCAGAAACATCAACGATGAAAGAGTCTGTAAGAGCCT 1296
 DB 527 CAAGATCATCTCTTCATCAGAAACATCAACGATGAAAGAGTCTGTAAGAGCCT 586
 QY 1297 CTACAGTATCTTTGGAGACATGAGCACTCTTCGAGAAAGACCTGTAAGAGCCT 1356
 DB 587 CTACAGTATCTTTGGAGACATGAGCACTCTTCGAGAAAGACCTGTAAGAGCCT 646
 QY 1357 ACCTGGTCTCTTGGTGAATGAGTATGATTTTCAACCCGACACCGTGTGCGCAA 1416
 DB 647 ACCTGGTCTCTTGGTGAATGAGTATGATTTTCAACCCGACACCGTGTGCGCAA 706
 QY 1417 TGGTGAATAACATTAACAAGATGAGAGGAGACATTAAGTATCAACCTTGAGGAGATG 1476
 DB 707 TGGTGAATAACATTAACAAGATGAGAGGAGACATTAAGTATCAACCTTGAGGAGATG 766
 QY 1477 GATGTTGGCTGGAATCATAGTATGATCTGCTGACATGCTTCACTCAACCTTA 1536
 DB 767 GATGTTGGCTGGAATCATAGTATGATCTGCTGACATGCTTCACTCAACCTTA 826
 QY 1537 ATAGTATCTGTTGTTGAGTACTGAGATGAGTGGTGTATATTTGGTACGTTGGAAGTG 1596
 DB 827 ATAGTATCTGTTGTTGAGTACTGAGATGAGTGGTGTATATTTGGTACGTTGGAAGTG 886
 QY 1597 ACAAGTCAATGTTATACCTAATGTTCTTGAAGTGGTGTGCTGCGGTTATCTCT 1656
 DB 887 ACAAGTCAATGTTATACCTAATGTTCTTGAAGTGGTGTGCTGCGGTTATCTCT 946
 QY 1657 CTACCGTGTGCTGACTTTCGCACTGTAAGTACCGTCTCGAGCAACATTTGCGAATC 1716

DB 947 CTAAACCTGCTGCTGACTTTCGCCATGTAAGTACCGTCTCGAGCAATTTCCGAATC 1006
 QY 1717 ATAAAGCTGCTGACGACCGTAGCTTAGCTTTCATTTGATTAATTCGTTTAC 1776
 DB 1007 ATAAAGCTGCTGACGACCGTAGCTTTCATTTGATTAATTCGTTTAC 1032
 QY 1777 AATCTCTGACGACCTAGTAACTAATTTTGTGTGTTTAAAGAGTGTACAGGAAG 1836
 DB 1033 -----AGAGTGTACAGGAAG 1051
 QY 1837 AAGATCAACAGGATTCAGAGGTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1896
 DB 1052 AAGATCAACAGGATTCAGAGGTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1111
 QY 1897 AAGCTCTCAAGCAACATCACTACTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1956
 DB 1112 AAGCTCTCAAGCAACATCACTACTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1171
 QY 1957 TTCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2016
 DB 1172 TTCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
 QY 2017 CCAGTCT 2076
 DB 1232 CCAGTCT 1291
 QY 2077 ATCTGTCAAGCATCATCTCCGAGTACAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2136
 DB 1292 ATCTGTCAAGCATCATCTCCGAGTACAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1351
 QY 2137 CGGCAAGCAAGTAGTGTGTAAGAGCTTCAGAAAGTCTAGGCTTGAAGTAAAGTAAAG 2196
 DB 1352 CGGCAAGCAAGTAGTGTGTAAGAGCTTCAGAAAGTCTAGGCTTGAAGTAAAGTAAAG 1411
 QY 2197 TGGAGCTCTGAGTGAAGTCAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 2256
 DB 1412 TGGAGCTCTGAGTGAAGTCAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 1471
 QY 2257 ATGAGTGTGCTCATGAGAGGCAAGAAAGTCTGAGAGGCGATAGGTTTGGCAGA 2316
 DB 1472 ATGAGTGTGCTCATGAGAGGCAAGAAAGTCTGAGAGGCGATAGGTTTGGCAGA 1531
 QY 2317 TCGCTTGGCTCTGCTGCTTAAAGTGAAGTGTGCTGAGAGGCAATGAGAGAGTGA 2376
 DB 1532 TCGCTTGGCTCTGCTGCTTAAAGTGAAGTGTGCTGAGAGGCAATGAGAGAGTGA 1591
 QY 2377 AGAAGCCAAACAGAAACATCTGGGTGATTCATCAACCGTTACCTGTGCTCTC 2435
 DB 1592 AGAAGCCAAACAGAAACATCTGGGTGATTCATCAACCGTTACCTGTGCTCTC 1650

RESULT 4

US-09-770-445-774/C
 ; Sequence 774, Application US/09770445
 ; Patent No. US20020023281A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goriach, Jörn
 ; APPLICANT: An, Yong-Olang
 ; APPLICANT: Hamillon, Carol M.
 ; APPLICANT: Price, Jennifer L.
 ; APPLICANT: Yu, Yang
 ; APPLICANT: Rameaka, Joshua G.
 ; APPLICANT: Page, Amy
 ; APPLICANT: Matthew, Abraham V.
 ; APPLICANT: Ledford, Brooke L.
 ; APPLICANT: Woessner, Jeffrey P.
 ; APPLICANT: Haas, William David
 ; APPLICANT: Garcia, Carlos A.
 ; APPLICANT: Kriker, Maja
 ; APPLICANT: Slader, Ted
 ; APPLICANT: Davis, Keith R.
 ; APPLICANT: Allen, Keith

QY	1865	GATTAAGTAGAGACTTTATGTGAAGCTTGGAGTGAAGCTCCCAAGACCAACATACACCTT	1922
Db	800	GATTAAGTAGAGACTTAATGTGAAGTTGGAGTGAAGCTCCCAAGACCAACATACACTACTT	741
QY	1925	AGGTCCTCTGTCCCTACCTTCTCCGAGCAGCTTCTCTTGTGCTCTCCGCG	1984
Db	740	AGGTCCTCTGTCCCTACCTTCTCCGAGAGCTTCTCTTGGCTGTCTCCGCG	681
QY	1985	AACCTTCTACCTGCGCCGCAAAAGCAGCAACCACTCTCTACTTCCGCGACCGC	2044
Db	680	AACCTTCTACCTGCTGCCCAAAAGCTCCACACACACTTCTCTACTTCCGCGACCGC	621
QY	2045	AAAAACCAATGGAATCAAGTCTTTCCTCCGATCTGTCCAAAGCCATATACCTCCGAGCTA	2104
Db	620	AAAAACCAATGGAATCAAGTCTTTCCTCCGATCTGTCCAAAGCCATATACCTCCGAGCTA	561
QY	2105	CAAGCTGCGCTTGAGAGATTTTGTTCACGCGGGGAAACAAAGTGTGCTGGAAGAGCT	2166
Db	560	CAAGCTGCGCTTGAGAGATTTTGTTCACGCGGGGAAACAAAGTGTGCTGGAAGAGNN	501
QY	2165	TCAAAAGAAATCTAGGCTTGAGTGAAGAAGAATAGAGAGCTTATAGAGTACACTTCACAG	2224
Db	500	NCAAAAGAAATCTAGGCTTGAGTGAAGAAGAATAGAGAGCTTATAGAGTACACTTCACAG	441
QY	2225	GTTTGGAAACACTTATGACGCTGGAATCTGTATGTAGTTGGCTTACATGGAGGCCAAGA	2288
Db	440	GTTTGGAAACACTTATGACGCTGGAATCTGTATGTAGTNNCTTACATGGAGGCCAAGA	381
QY	2285	AAGTGTCTGTAAGAGCGGATAGGGTTTGGCGAGATCCGTTTCGGTTCGTTTAAAGTGTAA	2344
Db	380	AAGTGTCTGTAAGAGCGGATAGGGTTTGGCGAGATCCGTTTCGGTTCGNNNTAAAGTGTAA	321
QY	2345	CAGTGTGCTGTGAAGGCAATAGAGAAAGTGAAGAAACCAACGAGACATCTTGGGT	2404
Db	320	CAGTGTGCTGTGAAGGCAATAGAGAAAGTGAAGAAACCAACGAGAACCAATCTTGGGT	261
QY	2405	GGATTGCATCAACCGTTACCTCTGGCTCTCTAAATATCATCTCTCTAAATTAATCA	2464
Db	260	GGATTGCATCAACCGTTACCTCTGGCTCTCTAAATATCATCTCTCTAAATTAATCA	201
QY	2465	GTAAGATCTCTAATTAATCTCCAAACCAAAAGATACAGTTGGTGGATGATGAGAGTTATTT	2524
Db	200	GTAAGATCTCTAATTAATCTCCAAACCAAAAGATACAGTTGGTGGATGATGAGAGTTATTT	141
QY	2525	ACGTATCATCTCGATCTCAAGTCTGTATTAAGATGGAATGGCTAGAGTCCGTTCAGCT	2588
Db	140	ACGTATCATCTCGATCTCAAGTCTGTATTAAGATGGAATGGCTAGAGTCCGTTCAGCT	81

1673 CTTTCGCCATGCTAAGTACCGCTTCGAGCACATTGTCCGAATCATTAAGGCTGCTGACGA 1732

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Db 936 CAGAGACGGTCTAAGTACAGGCTTGTACATGTACTCAGAGTACCGGTGAGCAGATGA 995
Qy 1733 CGTAGCTTCAAGCTTCAATTCATTTGGATTAATTCGTTTACATCTCTTGACCGAC 1792
Db 996 -----TAAAGCTTCCGTTGGTGTATATCAAGACGAGATGATACAGGGAG 1040
Qy 1793 TAGTAATAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1852
Db 996 -----TAAAGCTTCCGTTGGTGTATATCAAGACGAGATGATACAGGGAG 1040
Qy 1853 CAGAGGTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1912
Db 1041 AACCAGGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1100
Qy 1913 CATCACTACCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1972
Db 1101 TATCTACTATTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1155
Qy 1973 TTTGCTCCGCGAATCTCTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2032
Db 1156 -----TAAAGCTTCCGTTGGTGTATATCAAGACGAGATGATACAGGGAG 1155
Qy 2033 TTCCGCGACCGAATAACCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 2092
Db 1156 -----TAAAGCTTCCGTTGGTGTATATCAAGACGAGATGATACAGGGAG 1202
Qy 2093 CATCCGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 2152
Db 1203 TATCCGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1262
Qy 2153 GCTTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 2212
Db 1263 GATCATATGATGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1322
Qy 2213 GACACTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 2272
Db 1323 GACTTCAATGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1382
Qy 2273 GGAGGCAAGGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2332
Db 1383 TGAAGCAGGAAGGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1442
Qy 2333 TTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2392
Db 1443 ATTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1499
Qy 2393 CAATCCTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2434
Db 1500 CAGTCTGTGGGAAGTGTATGTATGACAAAGTATCCGGTAACTTT 1541

RESULT 6
US-09-938-842A-1598
: Sequence 1598, Application US/09938842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Kieps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: TITLE OF INVENTION: SAME, AND METHODS OF USE
: FILE REFERENCE: SCRIPT300-3
: CURRENT FILING DATE: 2001-08-24
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264,647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300,111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 1598

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: LENGTH: 1587
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-938-842A-1598

Query Match      10.0%; Score 278; DB 9; Length 1587;
Best Local Similarity 54.9%; Pred. No. 1.2e-47;
Matches 700; Conservative 0; Mismatches 430; Indels 144; Gaps 2;

Qy 1122 ACAAAGAAGTCTATAGTAACTAGCAGAAATATCAGGAAGTGTGAGGAAGACACTC 1181
Db 364 ACACAGAAACGTTATGACGCGTCTCAGCCTGTGCTATCTTACAGAAACCACTC 423
Qy 1182 GGTTCAGAAAGATCTTACACCTCAGCAGATGAGGAGACATACCTCCCAAGA 1241
Db 424 GCTTCCAAACAAATCTCTGACAGTTCGGTCTTGGCAAAACATTAATCTCCGGAG 483
Qy 1242 TCCATCTCTTCATCAGAAAACATAACAGATGAAAGAGTGTGGAAGAACCTCTACA 1301
Db 484 GCTCTTACGTCGCCGCTTATCTGTATGTCTGAAGCAAGGAAGAACCCGAGAG 543
Qy 1302 GTGATCTTGGACATGACGACACTCTTCGAGAGACACGTTAAACCTTAAGACGT 1361
Db 544 GTATGTTGGAGCTATGACGAGTGTGTGAAGAACCGGAGTGAATCTTAAGATAT 603
Qy 1362 GGTGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1421
Db 604 GGGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 663
Qy 1422 ATAAACATTAACATGAGAGGAAACATTAATTAATTAATTAATTAATTAATTAATTAAT 1481
Db 664 GTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 723
Qy 1482 TCGGCTGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1541
Db 724 AGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 783
Qy 1542 TATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1601
Db 784 TATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 843
Qy 1602 TCAATGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1661
Db 844 TCAATGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 903
Qy 1662 CGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1721
Db 904 CGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 963
Qy 1722 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1781
Db 964 GATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1001
Qy 1782 CTGACCGACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1841
Db 1002 -----CGAACAACAGAC 1014
Qy 1842 GACCAAGATTCAGAGGGTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1901
Db 1015 GACCAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1074
Qy 1902 CTCAAGCAACATCACTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 1961
Db 1075 CTCAAGCAACATCACTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 1134
Qy 1962 TTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2021
Db 1135 TTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1180
Qy 2022 TCTTCTCTACTTCCGACACCGCAAAACAAATGAATCAAGTCTCTCTCGATGTG 2081
Db 1181 ----- 1180

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QY 1362 GGTGTCCTGTGGTTAACTGTAGCAITTTCAACCCGACACCGTCTGTGTCCGCAATGGTG 1421

RESULT 8

US-09-883-797-1
 : Sequence 1, Application US/09883797
 : Patent No. US2002006123A1
 : GENERAL INFORMATION:
 : APPLICANT: Jaworski, Jan G.
 : APPLICANT: Post-Beltlemiller, Martha A.
 : APPLICANT: Todd, James
 : TITLE OF INVENTION: FATTY ACID ELONGASES
 : FILE REFERENCE: 07148/064001
 : CURRENT APPLICATION NUMBER: US/09/883,797
 : CURRENT FILING DATE: 2001-06-18
 : PRIOR APPLICATION NUMBER: 08/868,373
 : PRIOR FILING DATE: 1997-06-03
 : NUMBER OF SEQ ID NOS: 22
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 1
 : LENGTH: 1560
 : TYPE: DNA
 : ORGANISM: Arabidopsis thaliana
 : US-09-883-797-1

Query Match 9.7%; Score 269; DB 10; Length 1560;
 Best Local Similarity 55.2%; Pred. No. 8.4e-46;
 Matches 723; Conservative 0; Mismatches 430; Indels 156; Gaps 4;

QY 1123 CAAAAGAGAGTTCATAGAACTAGCGAGAAATCAGGAGAGTTGACGAGAGACACTCG 1182
 DB 392 CAGTAGATGCTCTTACGATGACGAGAAATGATCATCTACCGATGACACGGTTC 451
 QY 1183 GTTTCAGAGAGATGTTTACAGCCCTCAGGATAGCGAGACATACCTCCCAAGT 1242
 DB 452 AGTTCGCGAAGAGATTCGAAACCGGCGTTGGAGAGACATCTATCTGCCAGTG 511
 QY 1243 CCATCTTTCATCGAAGAAATACATGATGAGAGAGCGTGAAGAACTCTACAG 1302
 DB 512 GCATTAATTCAGCCCGCCGAGAGTAAATGTCAGAGCGACGCGGAGAGCTGAAGCG 571
 QY 1303 TGATCTTGGAGACATGACGAACTCTCGAAGAGACAGTGAAGAACTGAAGAGCTTG 1362
 DB 572 TTATGTTGAGAGCTTATGATCCCTCTCGAAGAAACCGGAAATTAACCGCGCAAGTCG 631
 QY 1363 GTGCTGTTGGTAACTGATGATTTCAACCGGACAGCGTCTGCGCATATGGTA 1422
 DB 632 GAATCTGATAGTAACTGAGCTTATTCATCCGAGCGCTCTCTACGCGATGATCG 691
 QY 1423 TAAACATTCAGAGAGAGAGAACTACTTACTTCAACCTTGAGAGAGTGGATGTT 1482
 DB 692 TGAACCATTCAGAGAGAGAGAACTCAAAAGTTTCAACCTTGAGAGAGTGGATGTT 751
 QY 1483 CGGCTGGAATCATAGCTATTTGCTGCTGACATGCTTCACTTCAACCTTAAAGTT 1542
 DB 752 CCGCGGATTAATCTCAATGATCTCGTCAACATCTCTCAAAAGAAACCTTAACTCT 811
 QY 1543 ATGCTGTTGTTGAGTACGAGATGGTGGGTAAATGTTAGTGGAGAGATGACAACT 1602
 DB 812 ACCTGTCGAGTGAAGAGAGAGAAATCAACCTTAACTGGTACTTGGAAATACCGGT 871
 QY 1603 CAATGTTATACCTAATTTGTTTCTTGAAGAGGTTGTTGCTGCGCTTATGCTCTTAAAC 1662
 DB 872 CAATGTCCTCTGCAATGATCTTCGAAATGGCGGAGCTGCGATCTCTCTTAAAC 931
 QY 1663 GTGCTGCTGACTTTCGCAATGCTTGAAGCTGCGAGCAGATGTTCCGAATCAAGG 1722
 DB 932 GCCGTCAAGACCGGAGAAAGTCAAGTACGCTGTCACAGCTGTTGCAACATTAAG 991
 QY 1723 CTGCTGACGAGCCGAGTTCAGGTTTCAATCTTTGGTATTAATGCTTTTAAACTCTC 1782
 DB 992 GATGAGCGACAGAACTACTACTT----- 1015
 QY 1783 TTGACCGAGCTAGTAACTAATTTTGTGTTTGTAGAGTGTGACGAGAGAAAGATG 1842
 DB 1016 -----GGGTGTACCAAGAGAAAGAGC 1036

QY 1843 AACAGGATTCAGAGGTTGAGATAGTAGAGACTTAATGGAAGTTGGAGTGAAGCTC 1902
 DB 1037 AGAGAGAGAACATCGGTGTCTTCTTACTAGAGAGCTCATGCTGTGCGCGAGACCTC 1096
 QY 1903 TCAAGACAAACATCATTACCTTAGTCTCTTCTCTTCTTCTTCTTCTTCTTCTTCT 1962
 DB 1097 TGAAGAACAAACATCAGACTTAGAGACGAGTTCCTTCAATGTCAGAGAGTGAATG 1156
 QY 1963 TCTTGTGCTGTGCTGCGCGAGACATTTTCACTGCTGCGCAAAAGCTCCACACCACTT 2022
 DB 1157 TCTTGTATTTCTTGTGCT----- 1173
 QY 2023 CTTTCTTACTTCCGACCGCAAAACCAATGATCAAGTCTTCTTCCAGTCTGT 2082
 DB 1174 -----AAAAGAGATGTTCAAGTAAAGTT----- 1200
 QY 2083 CCAAGCCATACATCCCGAGTACAAAGCTCGCTTCCAGCACTTTTGTCTCCAGCGCA 2142
 DB 1201 --AAACGTATATTCGAGATTCAGAGTTCGAGCACTTCTGATATTCACGACAGAG 1258
 QY 2143 GCAAGTAGTGTCTGAAAGAGCTTCAAAAGATCTAGGCTTGAGAGAGATATGAGG 2202
 DB 1259 GTAGAGGGTCTTAGAGAGAGTGAAGATCTGATCTCAAGATTTGGACATGAGAC 1318
 QY 2203 CTTTAGAGTACACTTCAAGAGTTTGAAGAACTTCTAGCAGTGAATCTGTATGACT 2262
 DB 1319 CTTCTAGATATCTTCTTCAAGATTTGTTGTAACCTTGAAGTCTGCTTGTATGAGA 1378
 QY 2263 TGCGTTACATGAGAGCGCAAGAGATGTTGTTAGAGGATGAGGTTTGGACATGCTT 2322
 DB 1379 TGCGTTATACCGAAGCTTAAAGGCTGCGGTTAAAGTGTGAGACCGCTTGGACATGCT 1438
 QY 2323 TCGGTTGCTTTTAAAGTGAAGTGTGTGGAAGCGAATGAGAGAGT---GAGA 2379
 DB 1439 TTGATGGGTTTCAAGATGATGATGCGGTTTGAAGAGCTTACGACCGGTTTCAAGCG 1498
 QY 2380 AGCCACCGAGAACATCTTGGTGTGATTCATCAACCTTATACCTGT 2428
 DB 1499 AGGAGATGACCGTAAATGCTTGGGCTGTTGATGATCAATATCCGCT 1547

RESULT 9

US-09-938-842A-1552
 : Sequence 1552, Application US/09938842A
 : Patent No. US20020160378A1
 : GENERAL INFORMATION:
 : APPLICANT: Harper, Jeff
 : APPLICANT: Kreps, Joel
 : APPLICANT: Wang, Xun
 : APPLICANT: Zhu, Tong
 : TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 : FILE REFERENCE: SCRI1300-3
 : CURRENT APPLICATION NUMBER: US/09/938,842A
 : CURRENT FILING DATE: 2001-08-24
 : PRIOR APPLICATION NUMBER: US 60/227,866
 : PRIOR FILING DATE: 2000-08-24
 : PRIOR APPLICATION NUMBER: US 60/264,647
 : PRIOR FILING DATE: 2001-01-16
 : PRIOR APPLICATION NUMBER: US 60/300,111
 : PRIOR FILING DATE: 2001-06-22
 : NUMBER OF SEQ ID NOS: 5379
 : SEQ ID NO 1552
 : LENGTH: 1563
 : TYPE: DNA
 : ORGANISM: Arabidopsis thaliana
 : US-09-938-842A-1552

Query Match 9.7%; Score 269; DB 9; Length 1563;
 Best Local Similarity 55.2%; Pred. No. 8.4e-46;
 Matches 723; Conservative 0; Mismatches 430; Indels 156; Gaps 4;

QY 1123 CAAAAGAGAGTTCATAGAACTAGCGAGAAATCAGGAGAGTTGACGAGAGACACTCG 1182


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Db 392 CAGTAGATTCGTTTGAGAGTACTGAGAGAAATGGATCATTCACCGATGACGGCTTC 451
Oy 1183 GTTTCAGAGAGAGATCTTACAGCCTCAGGCATAGGCGACAGACATACGTCCCAAGAT 1242
Db 452 AGTTCAGAGAAAGATCTCGAACCGGCGGCTTGGAGACAGACGTATCTGCGACGTG 511
Oy 1243 CCATCTCTTCATCAGAAAAACATTAACAGATGAAGAAGGTGTGAAGAAGCTCTACAG 1302
Db 512 GCATTAATCTCAAGCGCCCGGAGCTTAATATGTCAAGGACAGCTGCGAAGCTGAAGCCG 571
Oy 1303 TGAATCTTGGAGACACTCTCTGAGAGACAGACGTGAACCTTAAGACGTG 1362
Db 572 TTATGTTGGAGCCCTTAGATTCCTCTTGAGAAAAACCGGATTAACCGGCGGAGAGT 631
Oy 1363 GTGCTCTGTGTTAGCTAGTACATTTTCACCCGACACCGTGTGTCGCAAGGTGA 1422
Db 632 GAATCTTGATTAACAGCTGACATTCATCCAGCGCTCTCATAGCAGATGATCG 691
Oy 1423 TAAACCATTAACAAGATGAGAGGAGAACATTAATTAACAACCTTGAGGAGGATGTT 1482
Db 692 TGAACCATTAACAAGATGAGAGGAGAACATTAACAACCTTGAGGAGGATGTT 751
Oy 1483 CGGCTGGAATCATACCTATTTGATCTGCTGACATGCTTCAAGTCTAACCTTAATAGT 1542
Db 752 CGCGCGGATTAATCTCANTCGATCTCGCTAACATCTCTCAAGAAACCTTAATCTT 811
Oy 1543 ATGCTGTTGTTGAGTACTGAGATGATGTTGGTATTAATTTGTTAGCTGGGAACTGAC 1602
Db 812 AGCTGTGCTGTAGTACGAGAAACATTAACCTTAACCTGTTAGCTGGGAAATGACGGGT 871
Oy 1603 CAATGTTATACCTAATGTTCTTTAGATGGGTTGTTCTGCGCTTATGCTCTAAC 1662
Db 872 CAATCTCTCTGCAACTGATCTTCGATGGGCGAGCTCGATCTCTCTAAC 931
Oy 1663 GTGCTGCTGACTTTCGCCATGCTAGTAACTCTGAGACATTTGTCGAATCTAAG 1722
Db 932 GCGGCAAGACCGGAGAAAGTCAAAAGTACTGCTGTCACGCTGTCGAACATCAAAAG 991
Oy 1723 CTGCTGACGACCGTACTGCTGAGGTTTCATTTGTTATTAATTCGTTTCAATCTTC 1782
Db 992 GATCAGAGACACAAAGACTACAAATTTT----- 1015
Oy 1783 TTGACCGACCTGTAATATTTTGTGTGTTTGAAGTGTGACCGAAGAAAGATG 1842
Db 1016 -----GCGTGTACCGAAGAAAGACG 1036
Oy 1843 AACAGATTCAGGGGTTGAAGATAGTAGACTTAATGAAGTTGGAGTGAAGCTC 1902
Db 1037 AGAGAGAAACATGCGTGTCTTTAGCTAGAGAGCTCATGTCTGCGCGGAGAGCGTC 1096
Oy 1903 TCAACACAAACATCACTACTTACTGCTCTGCTTCTTCTTCTTCCGACAGCTTCTCT 1962
Db 1097 TGAACAAACAAACATCACTACTTACTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1156
Oy 1963 TCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2022
Db 1157 TCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1173
Oy 2023 CTTTCTACTTCCGCAACCGCAAAACCAATGAATCAAGTCTTCTCTCCGATCTGT 2082
Db 1174 -----AAAGAGATGTTCAAGTTAAAGTT----- 1200
Oy 2083 CCAAGCATATCCCGGACTCAAGCTGCTTGGAGCATTTTCTCTTCCAGCGGCA 2142
Db 1201 --AAACCGATATTCGCGGTTTCAAGCTGCTTGGAGCATTTCTTATTCAGCGAGAG 1258
Oy 2143 GCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2202
Db 1239 GTAGAGCGGTTTACAGAGTGCAGAAATCTTGATCTCAAAAGTTTGCAACATGAAC 1318
Oy 2203 CTTTAGATGACACTTCAAGAGTTTGAACACTTCTAGCAGTGAATCTGTATGAGT 2262

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Db 1319 CTTTGAATGACTTTCACAGATTTGTAACACTTCGAGTAGCTGCTTGGTATAGA 1378
Oy 2263 TGGCTTACATGAGGCGCAAGAAAGTCTCTAGAGCGATAGGTTTGGCAGATCGCTT 2322
Db 1379 TGGCTTATACCGAAGCTAAAGGCTGGGTTAAAGCTGGTGACCGACTTGGCAGATTCGT 1438
Oy 2323 TCGGCTGCTTAAAGTAAACAGTGTGTGAGGCAATGAGAAAGT---GAGA 2379
Db 1439 TTGATCGGCTTCAAGTATATAGTCCGTTTGGAAAGCTTACGACCGGTTTCACGG 1498
Oy 2380 AGCCAAACGAGAAACATTCCTTGGGTGATTTGATCAACCGTTACCTGT 2428
Db 1499 AGGAGATGACCGGTATGCTTGGCGCTGTTGATGATCAATATCCGCT 1547

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RESULT 10
US-09-883-797-9
; Sequence 9, Application US/09883797
; Patent No. US20020066123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Bellienmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-883-797-9

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Query Match 9.6%; Score 268.4; DB 10; Length 1611;
 Best Local Similarity 54.5%; Pred. No. 1,1e-45;
 Matches 722; Conservative 0; Mismatches 446; Indels 156; Gaps 3;

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Oy 1114 TTAGGTGACAAAGAGATTCATAGACTAGCGAAGAAATCAGGAGATTCGACGAG 1173
Db 440 TTGAGTTAGATGACGAAGTTTATGATCATTTAGTTGATGAAGTTTCAATAGAGT 499
Oy 1174 AGACACTGCGTTTCAAGAAAGAGATCTTAACAGCTTCAGGATAGCGACAGACATACG 1233
Db 500 CATCTTAAAGTTTACAGAGAAAGATTTGAACGTTCTGCTTAAAGAGAAAGACATTAATC 559
Oy 1234 TCCCAAGATTCATCTTTCATGCAAGAAACATATCAACAGATGAAGAAAGTCTGAGAAAG 1293
Db 560 TCCCTGAACCTTATCAATTTATTCCTCCAGAGGCTTCAGAGATGAGGCGCTGAGAGAAAT 619
Oy 1294 CCGCTACAGTGTCTTGGAGACACTAGACAACTTTCGAGAGACAGCTGTAACCTA 1353
Db 620 CTGAGAGAGTAAATGTTTGGTCTCTGATTAAGCTTTTCCAGATTAACAGATTAACCTTA 679
Oy 1354 AAGACGTGTGCTCTTGTGTTAACTGATGATTTTCAACCGGACACCGCTGTCTCG 1413
Db 680 GGAATATGCTGTGTTGTTGTTGAATTTAGCTTGTATTAATCTTACACCTGCTGTCTAG 739
Oy 1414 CAATGCTGATTAACATTAACAGATGAGAGGAAACATTAATTAACCTTGAAGGGA 1473
Db 740 CTATGATTTTAAACAAAGTATTAAGCTTAAAGGGAATTTAAAGATTTTAACTGTTGGA 799
Oy 1474 TGGAGATTCGCGTGAACATAGTATTAATGATCTCTGCTGACATGCTTCAAGTCAAC 1533
Db 800 TGGGCTGATGCTGTGTTATCTATGATTTACTTAAGATTAATGTTGCAAGTTCAAT 859
Oy 1534 CTAAATGATTAATGCTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1593
Db 860 GGAATACTTATGCTGTGTTGTTGTTAGTACGAGAACTTACTGAAATTTGATTTGGGA 919

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OY 1194 AGGATCTTACAGCCTCAGGATAGGCGAGACATAGTCCCAAGATCCATCTCTCA 1253
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DB 357 AGAATCTTGAACGTTCTGGCCCTGGTAGAGACTTGTCTCCCGCATTTATAT 456
OY 1234 TCAGAAACATVMAACAGCATGMAAGAGTGTGAAGAAGCCTCTACAGTATCTTTGA 1313
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 457 ATTCCTCCACACCAACACATGAGCCGGCTAGAACGAGCTCAATAGTTATCTTCGAG 516
OY 1314 GCATAGACGAACTCTTGAGAGAACACGVTAAACCTAAAGAGTGTGTCTGTGTG 1373
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 517 GCCATGAGACGATCTTTTCAAGAAACCGGTCTTAAACCTAAAGAGCTGACATCTTATC 576
OY 1374 GTTACTGTAGATTTTCAACCCGACCCGCTGTCCGCAATGTGTAACATATAC 1433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 577 GCAACTCTCTCTTCTTCTCTCCACACCATGCTCTCACTATGCTCAACAAATAT 636
OY 1434 AAGATGAGAGGAGACATCTTACTTATACAACTTGGAGGATGGATGTGCGCTGAATC 1493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 637 AAGCTTAGAGTAATATCAAGAGCTTCAATCTTTGGGGATGGCTGACGCCGGCCG 696
OY 1494 ATAGTATGATCTTCTGCTGACATGCTTCACTTAACCTTAATAGTTATGCTGTGT 1553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 697 ATCTAGTTGATCTAGCCCGGCACTTGTCTCAAGTTCATCCCAATCAATCAATCATC 756
OY 1554 GTGACTAGAGAGGTTGGGTATATGTTAGTCTGAGGAGAGACATGATGTTAT 1613
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DB 757 GTCACACGAGATCATATACGCTTAATTAATCAAGGACAGAGAGACCATGTTGTA 816
OY 1614 CCTAATGTTCTTATAGATGGGTTGTTCTGCGTTATGCTCTAACCCTGCTGTGAC 1673
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 817 CCCAATGTCTCTCCGATGGGTGGGAGCATACATGCTCAACGCCGGGTCTGAC 876
OY 1674 TTTGCCATGCTAATACCGTTCGACACATGTTCCGACTCATTAAGGCTCTGACAC 1733
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 877 CGGTGGCAGCCAAATACAGCTTTCACACCTGTCGCGACACACCGTGGCTGACGAC 936
OY 1734 CTAAGCTTCAAGTTCATTCATTTTGTATTAATTCGTTTACATCTCTGACGACT 1793
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 937 ----- 936
OY 1794 AGTAATATTTTGTGTGTTTTAGAGTGTGTACAGAGAGATGACAGATATC 1853
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 937 ----- AAGCTTCTACGTGTCTACGAAACAGAGAACAAAGACAC 981
OY 1854 AAGGGTTGAAGATTAAGTAGACTTAATGGAAGTTGAGGTTGAAGCTTCAAGCAAC 1913
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 982 GTTGGCATCACTTGTCCAAAGATCTCATGGCCATCGCGGTGAAGCCCTCAAGCCAAC 1041
OY 1914 ATCACTACCTAGTCTCTGCTCTTCTTACCTTCTCCGAGCAGCTCTCTTGTGTGT 1973
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1042 ATACACCAATATGTCCTTGTCTTACCGGGGTGAGAACAACTTCTCTCTCACGTCC 1101
OY 1974 TTGCTCCGCCGAACATCTCACCTGCGCAAAAGCTCCAAACCACTTCTCTACT 2033
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1102 CTAAATCGAGCTAAAT----- 1118
OY 2034 TCCGCCACCGCAAAACCAATGGAATCAAGTCTTCTCCGATCTGTCAAGCATAC 2093
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1119 -----CTTCMAACCGCAAAATGGAACCATAC 1143
OY 2094 ATCCGGACTACAGCTCGCTTGTGAGCATTTTGTCTCCAGCGGCAAGAAAGTAG 2153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1144 ATACGGATTTCAAGCTGCGCTTCAACACTTTTGCATTCACGCGAGAGCGGTG 1203
OY 2154 CTGGAAGCTTCAAAAGATCTAGCTTGAAGAGAAATATGAGGCTTCTAGAG 2213
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1204 ATCGAGAGCTCCAAAGAAATCTACACTATCAGAGAACAGCTTGAAGCCTCAAGAAT 1263
OY 2214 ACATCTCAGGTTTGGAAACCTCTAGCAATGGAATGTGTATGATGGCTTACATG 2273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1264 ACATCAATCGTTTGTGAACACGTCATCTTATGTTATGTTAGAGCTTACATAC 1323

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OY 2274 GAGCCAGGAAGATGTTCTGAGGCGATAGGTTTGGCAGATCGTTGCTGTGT 2333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1324 GAGCTTAAAGGAGATGAGAGCGCATCGCTTGGCAATGCGTTTGGAGTGT 1383
OY 2334 TTAAAGTATACAGTGTGTGTGGAAGGCAATGAGAGAGTGAAGGCAACAGAAC 2393
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1384 TTCAAGTATACGTCGCGCTGTGGAAGTAAACCGTACATTAAGA---CACTAAGAC 1440
OY 2394 AATCCTGGGTGATTCATCAACCGTTACCTGT 2428
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1441 GGACCATGTCGCAATGTTATCGACCGTTACCTGT 1475

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RESULT 13
US-09-892-325-3
; Sequence 3, Application US/09892325
; Patent No. US20020116735A1
; GENERAL INFORMATION:
; APPLICANT: Kunst et al.
; TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
; INVOLVED IN: Very Long Chain Fatty Acid Synthesis
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Klarkust Sparkman Campbell
; STREET: One World Trade Center, Suite
; 1600, 121 S.W. Salmon Street
; CITY: Portland
; STATE: OR
; COUNTRY: USA
; ZIP: 97204-2988
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3.5-inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Word97 & ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/892,325
FILING DATE: 26-Jun-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/058,947
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: David J. Earp, Ph.D.
REGISTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 5493-50032/DJE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-892-325-3
Query Match 8.9%; Score 247.4; DB 10; Length 1491;
Best Local Similarity 53.9%; Pred. No. 2.4e-41;
Matches 698; Conservative 0; Mismatches 441; Indels 156; Gaps 3:
OY 1134 TTCAATGAAGTACGCGAAGAAATCAGGAAAGTTCGACGAGACACTCGGTTCAAGAG 1193
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 328 TTCAATGAAGTACGCGTGTGATCCCAAGGACAGCCCTAAGAGGCTCAGTTCCAAATG 387
OY 1194 AGGATCTTACAGCCTCAGGATAGGCGAGACATAGTCCCAAGATCCATCTCTCA 1253
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 388 AGAATCTTGAACGTTTGGCTCGGTGAGAGACTTGTCTCCCTCCGCTATCAATAT 447
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1254 TCAGAAACATACAGATGGAAGAGTGTGGAAGAGCCTTACATGATCTTTGA 1313
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 448 ATTCCGCCACACCAACCATGGACGGGCTAGAACGAGCTCATAGTATCTTCGAG 507
 QY 1314 GCATAGACGAACTCTTGAGAGACACGTGTAAACCTAAGAGCTGTGCTCTTG 1373
 Db 508 GCCATTGGACCTTTTTCAGAAAAACCGTCTTAACCTAAAGACGTGACATCTTATC 567
 QY 1374 GTTAACCTAGATTTTCAACCCGACCGCTGCTGCGCAATGCTATTAACCATATC 1433
 Db 568 GTCAACTGCTCTCTTTTCTCCACACCATGCGCTCAGCTATGCTATCAACAAATAT 627
 QY 1434 AAGATGAGGGAACATCTTATAGTACCACTTGGAGGATGGATGTTGCGCTGAATC 1493
 Db 628 AAGCTTAGAGATTAATCAAGAGCTTCAATTTGCGGATGGGTGACGCGGCGCTG 687
 QY 1494 ATACCTATGATCTTCTGCTGACATGCTTACGTCAACCTAATAGTATGCTGTT 1553
 Db 688 ATTCAGATGATCTAGCCCGGACCTGCTCCAGTTCACCAATTCAAATGCAATCATC 747
 QY 1554 GTGAGTACTGATGTTGGGATTAATGTAACGTGGAAGTGAACATCATAGTTATA 1613
 Db 748 GTCAACGAGGATCATACCCCTAATTAATCAAGGCAAGAGAGACCATGTTGTTA 807
 QY 1614 CCTAATGTTCTTATAGATGGGTTGTTCCGTTATGCTCTGTAACCGTCTGCTGAC 1673
 Db 808 CCCAATTGCTCTTCCGATGGGTGCGGACCATACATGTCAAACGCGCGCTGAC 867
 QY 1674 TTTGCCATGCTAAGTACCGTCTGAGACATTTGCCAATCTAAGCTGCTGACGAC 1733
 Db 868 CGGTGGAGGCAATACACCTTTCCACCTGCTCCGACACACCGGTGGGCTGACGAC 927
 QY 1734 CGTAGTTCAGGTTTCAATTTTGGATTAATTCGTTTACAACTCTTGACCGACT 1793
 Db 928 ----- 927
 QY 1794 AGTAATAATTTGTGTTTATAGAGTGTACCAAGAGAGATGAACAAGATATC 1853
 Db 928 -----AAGTCTTCTACTGCTACGATACGAAAGAGAAAGAAAGAGACAC 972
 QY 1854 AAGGGTGAAGATTAAGTACGATTAATGAAATGGAGGTGAAGCTCTCAAGCAAA 1913
 Db 973 GTTGGATCAACTGTTCCAAAGATCATGCGCATGCGCGGTGAAGCGCTCAAGCAAA 1032
 QY 1914 ATCACTACTTATGCTCTGCTGCTACCTTTCTCCGAGGAGCTTCTCTTCTGCTGCT 1973
 Db 1033 ATCAACCAATAGTCTCTTGTGCTTACCGCGCTCAAGAACTCTCTTCTCAACGTC 1092
 QY 1974 TTGCTCCGCGCAATTTCTACCTGCTGCAAAAACGTCACAAACCATCTCTCTACT 2033
 Db 1093 CTAACTCGAGCTAAAT----- 1109
 QY 2034 TCCGCCACCCCAAAACCATGATCAAGTCTTCTCTCCATCTGTCACCAACCATAC 2093
 Db 1110 -----CTTCAACCCGAATGGAACCATATC 1134
 QY 2094 ATCCCGACTACAGCTCGCTTCGAGCATTTTGTTCACAGCGGGAAGCAAAAGTGTG 2153
 Db 1135 ATACCGGATTTCAAGCTGGCGCTTCGACACTTTTTCATTCACGAGAGAGGAGCGGTG 1194
 QY 2154 CTGGAAGAGCTTCAAAAGATCTAGGCTTAGTGAAGAGATATGAGGCTTCAAGATC 2213
 Db 1195 ATGAGAGAGCTCCAAAGATCTACACTATCAGGAGAACACGTTGAGGCTCAAGATG 1254
 QY 2214 ACGCTTACAGGTTTGAACACTTCTAGACAGTGGATCTGATGAGTTGGCTTACATG 2273
 Db 1255 ACGCTTACAGTCTTGTGTAACAGCTTCTTATGATGAGGCTTACATATC 1314
 QY 2274 GAGGCCAAGAAAGTGTCTAGAGGAGATAGGTTTGGAGATCGCTTCCGCTGCTGCT 2333
 Db 1315 GATCTTAAGAGGAGATGAGAGAGAGCGATCGCTTTGGCAAAATCGGCTTTGGAGTGT 1374
 QY 2334 TTTAAGTGAAGAGTGTGTTGGAAGCAATGAGAAAGTGAAGCAACCAAGAGAC 2393
 Db 1375 TTCAAGTGAAGTCTGCGCGGTGGAATATGTAACCGTACGATTAAGA---CACCTAAGGAC 1431

QY 2394 AATCCTGGTGGATTGCATCAACCGTTACCTGT 2428
 Db 1432 GGACCATGTGTCGATGTATGACCGCTTACCTGT 1466

RESULT 14

US-09-938-842A-569
 : Sequence 569, Application US/0993842A
 : Patent No. US20020160378A1
 : GENERAL INFORMATION:
 : APPLICANT: Harper, Jeff
 : APPLICANT: Kreps, Joel
 : APPLICANT: Zhu, Tong
 : APPLICANT: Wang, Xun
 : TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAININ
 : FILE REFERENCE: SRIPI300-3
 : CURRENT APPLICATION NUMBER: US/09/938, 842A
 : PRIOR FILING DATE: 2001-08-24
 : PRIOR APPLICATION NUMBER: US 60/227, 866
 : PRIOR FILING DATE: 2000-08-24
 : PRIOR APPLICATION NUMBER: US 60/264, 647
 : PRIOR FILING DATE: 2001-01-16
 : PRIOR APPLICATION NUMBER: US 60/300, 111
 : NUMBER OF SEQ ID NOS: 5379
 : SEQ ID NO 569
 : LENGTH: 1494
 : TYPE: DNA
 : ORGANISM: Arabidopsis thaliana
 US-09-938-842A-569

Query Match 8.9%; Score 247.4; DB 9; Length 1494;
 Best Local Similarity 53.9%; Pred. No. 2.4e-41;

Matches 698; Conservative 0; Mismatches 441; Indels 156; Gaps 3;

QY 1134 TTCAATAGACTAGCGAGAAATCAGGAGTTGACGAGAGACATCGGTTTCAAGAG 1193
 Db 328 TTCAATAGACTAGCGGTTGATCTCTCAAGAGCAAGCTTAAGAGCTGAGTTCAATG 387
 QY 1194 AGAATCTTACAGGCTCAGGATAGGCGAGAGACATACGTTCCAAATCATCTTCA 1253
 Db 388 AGAATCTTGAACGTTCTGCGCTGAGGAGACATGTTCCCTCCGCTATTCATTAT 447
 QY 1254 TCAGAAAACATTAACAGATTAAGAGAGTGTGAAGAGCTCTACAGTATTTGA 1313
 Db 448 ATTCCGCCACACCAACCATGAGCGGCTAGAACGAGCTCATAGTATCTTCGAG 507
 QY 1314 GCATAGACGAACTCTTGAGAGACACGTGTAAACCTAAGAGCTGTGCTCTTG 1373
 Db 508 GCCATTGGACCTTTTTCAGAAAAACCGTCTTAACCTAAAGACGTGACATCTTATC 567
 QY 1374 GTTAACCTAGATTTTCAACCCGACCGCTGCTGCGCAATGCTATTAACCATATC 1433
 Db 568 GTCAACTGCTCTCTTTTCTCCACACCATGCGCTCAGCTATGCTATCAACAAATAT 627
 QY 1434 AAGATGAGGGAACATCTTATAGTACCACTTGGAGGATGGATGTTGCGCTGAATC 1493
 Db 628 AAGCTTAGAGATTAATCAAGAGCTTCAATTTGCGGATGGGTGACGCGGCGCTG 687
 QY 1494 ATACCTATGATCTTCTGCTGACATGCTTACGTCAACCTAATAGTATGCTGTT 1553
 Db 688 ATTCAGATGATCTAGCCCGGACCTGCTCCAGTTCACCAATTCAAATGCAATCATC 747
 QY 1554 GTGAGTACTGATGTTGGGATTAATGTAACGTGGAAGTGAACATCATAGTTATA 1613
 Db 748 GTCAACGAGGATCATACCCCTAATTAATCAAGGCAAGAGAGACCATGTTGTTA 807
 QY 1614 CCTAATGTTCTTATAGATGGGTTGTTCCGTTATGCTCTGTAACCGTCTGCTGAC 1673
 Db 808 CCCAATTGCTCTTCCGATGGGTGCGGACCATACATGTCAAACCGCGCTGAC 867

OY	1674	TTTGCCATTCGTATGATACCGCTCGACGAATTTGCGAATCTATATAGGGCTGACGAC	1733
Db	868	CGGTGGCGAGCCAAATATACAGCTTTCCCACTCGTCCGACACACCGGTGGCTGACGAC	927
OY	1734	CGTAGCTTCAGGTTCATTCATTTTGGTATTAATTCGTTTACAAATCTTGACCGCACT	1793
Db	928	-----	927
OY	1794	AGTAACTAATTTTGTGTGTTTATAGAGTGTGACGAGAGATGAAACAGATTC	1853
Db	928	-----AAGCTTTCTACTGTGTCTACCAACAGGAACAAAGAAGGACAC	972
OY	1854	AAGGGTTGAAGATAAATAGAGACTTAAATGGAAGTTGAGTGAAGTCTCCAGACAAAC	1913
Db	973	CTTGCACTACATCTTGTCACAAAGATCTATGCGCATGCGCGGTGAAGCCCTCAAGGCAAC	1032
OY	1914	ATCACTACCTTAGGTGCTCTGTGCTCTACCTTCTCCAGAGAGCTTCTCTTGTGTCT	1973
Db	1033	ATCAACAACAATAGTCTCTTGTTGCTCTACCGCGGTCAACAACACTTCTCTTCACCTCC	1092
OY	1974	TTTGCTCCGCGCAACATCTCACCTGTGCGCAAAAGTCCAAACCAACACTCTCTCTACT	2033
Db	1093	CTAATCGACCTAAAT-----	1109
OY	2034	TCCGCAACCGCAAAAACCAATGGAATCAAGTCTCTCTCCATCTGTCCAAAGCATAC	2093
Db	1110	-----CTTCAACCCGAATGGAACCATAC	1134
OY	2094	ATCCCGGACCTACAGCTCGCCTTGACGACATTTTGTTCACGCGGCAACAAGTAGTG	2153
Db	1135	ATACCGGATTTCAAGTGTGCGCTTGGAACACTTTTGCAITTCACGAGAGGACAGCGGTG	1194
OY	2154	CTTGAAGACTTCAAAAGATCTAGGCTTGAGTGAAGAGAATATGAGGCTTCTAGAGT	2213
Db	1195	ATCAGACGAGCTCAAAAGATCTCAACTATCAGAGAGAACAGCTTGAGCGCTCAAGATG	1254
OY	2214	ACACTTCACAGTGTGGAACACTCTAGACAGTGGATCTGATGTAGTGGCTTACATG	2273
Db	1255	ACACTACTCTCTTTTGGTAACAGCTCACTTCATCGTTATGTAGTCGAGCTTAGCTATAC	1314
OY	2274	GAGGCCAAGGAAGATGTTCTGTAGAGGCGATAGAGTTTGGCAGATCGCTTTCGGTCTGAT	2333
Db	1315	GAGTCTAAAGGGAATATGAGGAGAGGGGATGGCTTTGGCAAAATCGCGTTTGGAGAGGT	1374
OY	2334	TTTAAAGTGTAACTGTGTGTGTGAGAGCAATGAGAAAGTGAAGAACCAACGAGGAC	2393
Db	1375	TTCAAGTGTAACTGTGCGGTGTGGAATGTAAACGATGATTAAGA---CACTTAAGGAC	1431
OY	2394	AATCCTTGGGTGATTCATCAACCGCTTACCCTGT	2428
Db	1432	GGACCATGTCCGATGTATCGACCGGTACCCTGT	1466

RESULT 15
 US-09-892-325-2
 Sequence 2, Application US/09892325
 Patent No. US20020116735A1
 GENERAL INFORMATION:
 APPLICANT: Kunst et al.
 TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
 Involved In Very Long Chain Fatty Acid Synthesis
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Klargiust Sparkman Campbell
 Leigh & Whinston, LLP
 STREET: One World Trade Center, Suite
 1600, 121 S.W. Salmon Street
 CITY: Portland
 STATE: OR
 COUNTRY: USA
 ZIP: 97204-2988
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk, 3.5-inch

[illegible]

OY 1794 AGTAACTAATTTGTGTGTTTAAAGAGTGTATACAGAGAGATGACAGGATTC 1853
DB 986 -----AAGCTTTTCTACTGTGTCTACGAAAGAGAGACAAAGAGAGACAC 1030
OY 1854 AAGGGTTGAATAGTAACTTAATGAAAGTGGAGTGAAGCTCTCAAGACAAC 1913
DB 1031 GTTGGCATCACTTGTCCAAAGATCTCATGCGCATCGCGTGAAGCCCTCAAGGCAAC 1090
OY 1914 ATCACTACTTAGTGTCTGTGCTTCTGCTACCTTCTGAGAGAGTGTCTTCTTGTGCT 1973
DB 1091 ATCACACATAGTGTCTTGTGCTTCTGCTACCGGCTGAGAACTTCTTCTTCTCAGTCC 1150
OY 1974 TTGCTCCGCCGGAATCTCTACCTGTGCAAAAGCTCCACAACACTTCTTCTACT 2033
DB 1151 CTAAATGGAGCTAAAT----- 1167
OY 2034 TCCGCCACCGCAAAACCAATGAAATCAAGTCTTCTTCCGATCTGTCAAGCCATAC 2093
DB 1168 -----CTCAACCCGAAATGAAACCATAC 1192
OY 2094 ATCCGGACTACAGGTGCTTCCAGCATTTTGTCTTCCAGCGGCAAGCAAGTAGTG 2153
DB 1193 ATACGGATTTCAGGTGCTTCCAGCATTTTGTCTTCCAGCGGCAAGCAAGTAGTG 1252
OY 2154 CTTGAAGAGCTTCAAAAGATCTAGGCTTGAAGAGATATGAGAGCTTCTAGATG 2213
DB 1253 ATCGAGAGACTCCAAAAGATCTACAACTATCAGAGAAACAGTGTAGGCTCTAAGATG 1312
OY 2214 ACACCTTACAGTGTGGAACCTTCTAGCAGTGAATCTGTATGAGTGTGCTTACATG 2273
DB 1313 ACACATCATCGTTTGTGTACAGCTCATCTTCACTGTATGTGTACGAGCTTAGCTACATC 1372
OY 2274 GAGGCCAAGGAAGTGTGTGAGAGCGATAGGAGTTTGGCAGATCGTTTGGTCTGTGT 2333
DB 1373 GAGTCTAAAGGAGAGATGAGAGAGCGCATTCGCGTTTGGCAATTCGCTTTGGAGTGTGT 1432
OY 2334 TTAAAGTGTACAGTGTGTGTGGAAGGCAATGAGAGAGTGAAGAGCCAAACAGGAAC 2393
DB 1433 TTCAGGTGTACTGTGCGCTGTGGAATGTAAACCGTACGATTAAGA---CACCTAAGGAC 1489
OY 2394 AATCCTTGGGTGATTTGCATCAACGTTACCTGT 2428
DB 1490 GGACCATGTGTCGATTGTATGACCGTTACCTGT 1524

Search completed: May 10, 2003, 22:59:01
Job time : 383 secs